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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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## ALIGNMENTS

Qy Db	Db Qy Db	,	REQUESTION OF THE PROPERTY OF
121 NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH 180 		atch 100.0%; Score 3019; DB 2; Length 594; cal Similarity 100.0%; Pred. No. 1.2e-118; 594; Conservative 0; Mismatches 0; Indels 0; Ga	RESULT 1  Q93QY4 PRELIMINARY; PRT; 594 AA.  AC Q93QY4;  DT 01-DEC-2001 (TrEMBLrel. 19, Created)  DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  DE NHAA OUTER MEMBRANE PROTEIN.  GN NHAA.  OS Neisseria meningitidis.  OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  OX NCBI_TaxID-487;  RN [1]  RC STRAIN-EG327;  RP SEQUENCE FROM N.A.  RT "Identification and characterization of a gene encoding a novel outer  RT membrane protein of Neisseria meningitidis.";  RL Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.  DR EMBL; AF157605; AAK68866.1; -  DR EMBL; AF157605; AAK68866.1; -  DR EMBL; AF157605; AAK68866.1; -

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X MEDLINE-20175756; PubMed=10710308;

AP Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

AR Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

AG Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

AR Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

AR Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

AB Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

AR Moxon E.R., Grandi G., Rappuoli R.,

AN Moxon E.R., Grandi G., Rappuoli R.,

AN Moxon E.R., Grandi G., Rappuoli R.,

Yidentification of Vaccine Candidates Against Serogroup B

Whole-Genome Sequencing.";

EMBL, AF226376; AAF42518.1;

EMBL; AF226376; AAF42518.1;

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01-OCT-2000 (TremBLrel. 15, Last sequence update)
01-MAR-2001 (TremBLrel. 16, Last annotation update)
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  NTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGDTTVH
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Pred. No. 5.6e-115;
5; Mismatches 12;
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                                                                                                                                                                                 MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecch
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., N
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                       Meningococcus by Whole-Genome Science 287:1816-1820(2000). EMBL; AF2256379; AAF42528.1; -. SEQUENCE 594 AA; 62114 MW;
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                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
Bacteria; Proteobacteria;
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(TrEMBLrel. 16, Last annotation
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01-OCT-2000 (TrE
01-OCT-2000 (TrE
01-DEC-2001 (TrE
OUTER MEMBRANE F
  "Identification and characterization of a gent membrane protein of Neisseria meningitidis."; submitted (JUN-1999) to the EMBL/GenBank/DDBJ EMBL; AP226388; AAF42517.1; -.. EMBL, AP226388; AAF42507.1; -. EMBL, AP226388; AAF42507.1; -. EMBL, AP57604; AAF468865.1; -. SEQUENCE 594 AA.
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Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BZ198, AND 297-0;
MEDLINE=20175756; PubMed=10710308;
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X MEDILINE-20175756; PubMed=10710308;
A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
A Comanducci M., Junnings G.T., Baldi L., Bartolini E., Capecchi B.,
A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.;
T "Identification of Vaccine Candidates Against Serogroup B
T Meningococcus by Whole-Genome Sequencing.";
L Science 287:1816-1820(2000).
C SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Q9JPR9;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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Bacteria;
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                                                                                                                                                        SEQUENCE FROM
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MEDINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
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01-OCT-2000
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P SEMPLEMENTS;
(C STRAIN=NCHIS;
(XX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
RA Comanducci C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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GNA992 OR NHHA.
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EMBL; AF157607; AAK68868.1; --
SEQUENCE 598 AA; 62763 MW; E
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                       Bacteria; Prote NCBI_TaxID=487;
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Neisseria
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MEDLINE-20175756; PubMed-10710308; Pizza M., Scarlato V., Masignani V., Comanducci M., Jennings G.T., Baldi Galeotti C.L., Luzzi E., Manetti R.,
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01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
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EMBL, AF226371; AAF42520.1; -
        Neisseria meningitidis.
Bacteria; Proteobacteria;
NCBI_TaxID=487;
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GNA992 OR NHHA.
Neisseria meningitidis.
Bacteria; Proteobacteria; beta
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B
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EMBL; AF226378; AAF42527.1; -. SEQUENCE 590 AA; 61661 MW; 8AA476AC30
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----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTT 174
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
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"Identification and characterization of a gene
membrane protein of Neisseria meningitidis.",
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ o
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A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.;
T "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
R EMBL: AF226366; AAF42515.1;
Sequence 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;
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RC STRAIN-MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

TT Meningococcus by Whole-Genome Sequencing.";

L Science 287:1816-1820(2000).
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Tidentification and characterization of a gene encoding a nove.
Tidentification of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF226375; AAF42524.1;
R EMBL; AF226376; AAF42519.1;
EMBL; AF226370; AAF42519.1;
EMBL; AF226374; AAF42519.1;
EMBL; AF26374; AAF42523.1;
EMBL; AF26374; AAF42523.1;
TIGE; NMB0992;
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Q9JR18;
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                                                                                                                                                                                                                                                                                                                                  Complete SEQUENCE
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MEDLINE-20175755; PubMed-10710307;
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Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision;
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Bacteria;
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peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jenr Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jenr Peak I.R., Station and characterisation of a gene encoding membrane protein of Neisseria meningitidis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFL5375; AAK09243.1;
SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
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O1-DEC-2001 (TrEMBLrel. 19, La
NHHA OUTER MEMBRANE PROTEIN.
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EMBL: AF157606; AAK68867.1; -. SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;
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Bacteria; Proteobacteria;
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                   TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKDK
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                                                                -NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD
                                                                                                                                                                                                   Conservative
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                                                              KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476
                                                                                              DANKPYRITNYAPGYKEGDYTNYAQLKGVAQNINNHIDNYDGNARAGIAQAIATAGLYQA 536
YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
        YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                               KDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 533
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Search completed: July 3, 2002, 08:28:43 Job time: 1164 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 3, 2002, 08:12:18; Search time 95.27 Seconds (without alignments) 596.083 Million cell updates/sec Run on:

US-09-771-382-5 2999 1 MNEILRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 591 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	n NMB0992	probable surface f	adhesin homolog HI	surface protein XF	probable autotrans	surface protein XF	probable adhesin Z	probable adhesin E	probable surface p	surface-exposed ou	high-molecular-wei	hypothetical prote	high-molecular-wei	probable adhesin h	ABC-type transport	hypothetical prote	filamentous hemagg	hemolysin [importe	hypothetical prote	AidA-I adhesin-lik	probable adhesin Z	hemagglutinin/hemo	sapB protein - Cam	surface-array prot	hemolysin A precur	probable RTX famil	adhesin AIDA-I pre	probable adhesin P	ydeK protein - Esc
SUMMARIES	ID	8113	A81888	164138	D82671	AC0976	A82615	A86036	н91188	AH0110	C82672	A43855	G64964	B43855	AF0394	C48399	F90696	T31102	AI0452	T31105	D90803	н85611	T09083	140711	A56143	A35140	B85547	S28634	3	A64905
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	Score	86	2445.5	9	393	375	372.5	368	3	332.5	239.5	230.5	228.5	225	219	2	213.5	212.5	212	211.5	209	209	209	208.5	207.5	207.5	207		•	199
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,	9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.3	6.3
,	199	197	197	196.5	196.5	196	195	194.5	193.5	192.5	191.5	191.5	191	190.5	190	189.5
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## ALIGNMENTS

 R C C C C C C C C C C C C C C C C C C C	RESULT 1 GB1133 adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup C; Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: GB1133 R;Tettelin; H.; Sanders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E. Hicker, P. Y. 10-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4-4	<pre>(strain MC58 serogroup B) #text_change 19-Jan-2001 fries, A.C.; Nelson, K.E.; Eisen, relaischmann P. D. Dougherty B.</pre>
 ri Soci	ntracy, bir, marty oil, sarabers, bir, marty oil, wastgani, v. r.	, V.; Masignani, V.; Pizza, M. C. M. Movon R. B. Rannioli, R.
A A A	A/Auchous: Grand, G.; Sun, L.; Suntun, n.C.; Flager, C.m.; Mozon, E.N.; Reprostry A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS A;Reference number: A81000; MUID:20173755 A;Accession: G81133	ngitidis serogroup B strain MC58.
 A A A	A;Status: preliminary A;Molecule type: DNA A;Redidner: 1-591 <pff< td=""><td></td></pff<>	
AA	A.Cross-references: GB.AE002450; GB.AE002098; NID:g7226229; PIDN:AAF41395.1; A.Experimental source: serogroup B, strain MC58	7226229; PIDN:AAF41395.1; PID:g722
A);	C;Generics: A;Gene: NMB0992	
 <u>.</u>	% % % %	Length 591;
 •	Matches 588; Conservative I; Mismatches	2; Indels U; Gaps U;
 QY		
 qa	Db 1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLA	LLFATVQASANNEEQEEDL 60
Qy	61	
 qu	Db 61 YLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ	VLTAREITLKAGDNIKIKQ 120
 QY	121	
 Dp	Db 121 NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN	ILNFAKETAGTNGDTTVHLN 180
 Qy	181	GWNIKGVKPCTTASDNVDF 240
 QQ	Db 181 GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF	GWNIKGVKPGTTASDNVDF 240
Qy	Qy 241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS	KEKDGKLVTGKDKGENGSS 300
QΩ	Db 241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS	KEKDGKLVTGKDKGENGSS 300
 ΟY	Qy 301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV	VTSGTNVTFASGKGTTATV 360
 qa	Db 301 TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNYTFASGKGTTATV	VISGINVIFASGRGTTATV 360

361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 420

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Surface protein XF1529 [imported] - Xylella fastidiosa (strain 995c)
C;Species: Xylella fastidiosa
C;Species: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82671
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
                                                                                                                                                                                                                                                             adhesin homolog H1732 - Haemophilus influenzae (strain Rd KW20)

C;Species: Haemophilus influenzae
C;Accession: I64138
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
C;Accession: R.D.; Scott, J.; Shirtey, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
C;Gocayne, J.D.; Scott, J.; Shirtey, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Recession: I64138
A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732
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                 1 MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLSATVQAINDAGTFVKVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 NLKIK--QNGTNFTYSLKKDLTDLTSVGTEKLSFSAN-----GNKVNITSDTKGLNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 KETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 KGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKD
                                                                      531 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 20.0%; Score 600; DB 2; Length 29 Best Local Similarity 44.7%; Pred. No. 1.8e-23; Matches 144; Conservative 39; Mismatches 91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-298 <TIGR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-592 <PAR>
A;Cross.references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
A;Experimental source: serogroup A, strain 22491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                       probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 224) C;Species: Neisseria meningitidis (5-May-2000 #text_change 02-Feb-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                    S.R.; More
Rajandream
                                                                                                                                                                                                                                                                                                                                                                                                          R; Parkhill, J; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mor.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrean Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Nelsseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8;
                                                                          Q-----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNG 173
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Best Local Similarity 83.7%.
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2059 <SIM>
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Prismpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Carraro, D.M.; Carrer, F. Sarneto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramee, E.E.; Laigrichado, M.A.; Madeira, A.M.Bh.; Matsukuma, A.Y.; Menck, C.F.M.; Marques, M.V.; Martins, F.G.; Nuthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracaca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D. A; Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Reinako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zanesin, A.S. A.C.R., Salva, V.S., Verjovski-Almeida, S.; Vettore, A.L.; Zanesin, A.S. A.C.R., Salva, Verjovski-Almeida, S.; Vettore, A.L.; Zanesin, A.L.; Zanesin, A.S. A.C.R., Salva, Verjovski-Almeida, S.; Vettore, A.L.; Zanesin, A.L.; Zanesin, A.J. Verjovski-Almeida, S.; Vettore, A.L.; Zanesin, A.L.; Zanesin, A.J. Verjovski-Almeida, S.; Vettore, A.L.; Zanesin, A.L.; Zanesin, A.J. Verjovski-Almeida, S.; Vettore, A.L.; Zanesin, A.L.; Zanesin, A.J.; Zanesin, A.J.; Zanesin, A.L.; Zanesin, 
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5.9e-12;
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probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova Cispecies: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Species: Salmonella enterica serovar Typhi C; Date: 09-Nov-2001 #text_change 09-Nov-2001 #text_change 09-Nov-2001 R; Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard, D; Wain, J.; Church th, T; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.
Nature 413, 848 e852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: AB0502; PMID:11677608
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-1107 cPAR>
A; Residues: 1-1107 cPAR>
A; Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.5%; Score 375; DB 2; Length 1107; Best Local Similarity 21.1%; Pred. No. 2.1e-11; Matches 176; Conservative 106; Mismatches 238; Indels 314;
272 VKIGAKTSVIKEKDGKLVTGKDK------GENGSSTDEG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NEKVDQNT-----
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Db 876 YFKTNTDGADANAQGADSVAIGSGSIAAAENSVALGTNSVADEANTVSVGSSTQQRRI 933  Qy 482 TNVAPGVKEGDVTNVAQLK	237NUDFVRTYDTVEFLSADTRTTTVNVESKDNGKKTEVKIGAKTSV 28
Surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C;Accession: A82615 R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Note: for a complete list of authors see reference number A59328 below A;Note: for a complete list of authors see reference number B59328 below A;Note: preliminary A;Notecasion: A82615 A;Status: preliminary A;Notecule type: DNA A;Residues: 1-1190 <sim></sim>	Qy         456 ADAPTLSVGDALNVGSKKDNKPV
A;Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.E.; Decena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E.A.; Atuthors: Martins, E.M.F.; Matsukuma, A.V.; Manck, C.E.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvaineria, A.S.; Vettore, A.L.; Z.A; Reference number: A59328 A;Contents: annotation A;Gene: XF1981	RESULT 7 886036 probable adhesin 25029 [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C; Species: Escherichia coli C; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: A86036 R; Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 A; Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A; Reference number: A85480; MUID:21074935; PMID:11206551 A; Reterence number: A86036 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1588 <sto> A; Cross.references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP: A; Experimental source: strain 0157:H7, substrain EDL933 C; Genetics: A; Gene: Z5029</sto>
Query Match         12.4%; Score 372.5; DB 2; Length 1190;           Best Local Similarity 23.6%; Pred. No. 3.1e-11;         3.1e-11;           Matches 168; Conservative 88; Mismatches 242; Indels 213; Gaps 28;           Qy 17 VVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVLRTVAV 71	Ouery Match  Best Local Similarity 23.3%; Pred. No. 7.6e-11;  Matches 162; Conservative 99; Mismatches 280; Indels 154; Gaps 25;  Qy 31 SATVKTAVLATILFATVQASANNEEQEEDLYLDPVLRTVAVLIVNSDKEGTGEK-EKVEE 89

Db 1154 YRQIINVADGSEAHDAVT-VROLONAIGAVATTPTKYFHANSTEEDSLAVGTD 1205  Qy 271 EVKIGAKTSVIKEKDGKLWTGKDKGENGSSTDEEGGL 307  Db 1206 SLAMGAKTINGDKGIGIGYGAXVDANALNGIAIGSNAQVIHVNSIAIGNGSTTRGAQT 1265  Qy 308 VTAKEVIDAVNKAGWRWKTTTANGOTGQADKFETYTSGTNVTFASGKGTTATY 360  1206 NYTAYNMDAPQNSVGEFSVGSADGOROITNVAAGSADTDAVNVGQLKYTDAQV 1318  Qy 361 SKDDGNITVW	RESULT 9 AH0110 probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain C092) C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 C;Accession: AH0110 R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. R; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.M.; Davis, P.; Dougan, G. 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-658 <kur> A;Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:915978974; GSPDB:GN00175 C;Genetics: A;Genetics:</kur>	Ouery Match Best Local Similarity 24.3%; Pred. No. 1.5e-09; Matches 155; Conservative 86; Mismatches 241; Indels 155; Gaps 29; Matches 155; Conservative 86; Mismatches 151; Indels 155; Gaps 29;  QY 27 TKRASATWATAVLATLEATVOASANNEEDEEDLYLDPVLRTVAVLIV 74
Db 1154 YROIINVADGSEAHDAVT-VROLONAIGAVATTPTKYFHANSTEEDSLAVGTD 1205  Qy 271 EVKIGAKTSVIKEK	RESULT 8 H91188 Probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RI C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Barbul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001 C; Accession: H91188 R; Hayashi, T; Makino, K; Ohnishi, M.; Kurokawa, K; Ishii, K; Yokoyama, K.; Han, C. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhaqic Escherichia coli O157:H7 and ge A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Recession: H91188 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1588 CHAY> A; Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g13363955; GSPDB:GN00154 A; Experimental source: strain 0157:H7, substrain RIMD 0509952 C; Genetics: A; Gene: ECs4480	Ouery Match  12.3%; Score 368; DB 2; Length 1588;  Best Local Similarity 23.3%; Pred. No. 7.6e-11;  Matches 162; Conservative 99; Mismatches 280; Indels 154; Gaps 25;  Qy 31 SATVKTAVLATLEATVQASANNEEGEEDLYLDPVLRTVAVLIVNSDKEGTGEK-EKVEE 89

Db 64SPAMVTASKVMVAHVDSQVNRTADRIPTGDGSELMTHMALDWKFFPFGNNSIA 116 OV 96YFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKV 153		Qy 154 NITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAA 213 		Qy 250LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKD 293  Qy 250LSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKD 293  1		Qy 333 TGQADKFETVTSGTNVTFASGKGTTAT-VSKDDQGNITVMYDVNVGDALNVNQLQNSG 389 	QY 390 WNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINACNNIEITRNGKNIDIATS 442 :	QY 443 MTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQ 498 : :  :   :    :    :    :    :    :	QY 499 LKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIG 544	Qy 545	DD 611 NAIGSSVLGVDSRARGINSTALGRUSNAIGDGSVSLGFNSFYRUSGERGVALGIDAGVSS Ov 583 a-gagydy 589	Db 671 KDSIALGY 67	RESULT 11 A43855		C;Accession: A43855 R;Barenkamp, S.J.; Leininger, E. Infect. Immun. 60, 1302-1313, 1992			A;Cross-references: GB:N088/05, GB:N884616; NID:94/57/0; PIDN:AAAAU527.1; PID:94/57/1. A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:89235, NCBIP:89239)	Query Match 7.7%; Score 230.5; DB 2; Length 1536; Best Local Similarity 22.3%; Pred. No. 0.00061; Matches 133; Conservative 86; Mismatches 228; Indels 149; Gaps 26;	Qy 40 atilfatvqasanneeqeedlyidpvirtvavlivnsdkegtgekekveensdwavyfne 99
OY 225 IKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTVNVESKDNGKKTEVKIGAKT 278  1	QY 279 SVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRWKTTTANGQTGQADK 338    1	OY 339 FETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNOLQNSGWNLDSKAVA 398  DS 408 TVSCKGNTAT CETT PITT	399 GSSGKVISGNVSPSKGKMDETVNINAGNNI-EITRNGKNIDIATSMTPQFSSVSLGAG	456 ADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVINVAQLKGVAQN	506LINNRIDANDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGY 1	555 AIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591	10	CB16/2 Surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000	C;Accession: C&20/2 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.	A; Reference number: A82515; MUID:20365717 A; Note: for a complete list of authors see reference number A59328 below A; Accession: C82672	A;Status: preliminary A;Molecule type: DNA A;Dosidius: 1-100A CTMS	A; Residues: 1-1004 <51m. A; Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001 A; Experimental source: strain 9a5c A; Experimental source: strain 9a5c A; Experimental source: Strain 8a5c A; Experimental source	Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000	A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H	A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak	A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A;Reference number: A59328 A;Contents: annotation	. C;Genetics: A;Gene: XF1516	Query Match 8.0%; Score 239.5; DB 2; Length 1004; Best Local Similarity 22.1%; Pred. No. 0.00012; Matches 161; Conservative 97; Mismatches 277; Indels 193; Gaps 34;	QY 2 NEILRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEE 55	Qy 56 QEEDLYLDPVLRTVA-VLIVNSDKEGTGEKEKVEENSDWAV 95

OY 119 KONGTNETYSLKKDLTDLTSVGTEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTTVH 178	RESULT 13 B4385 high-colecular-weight surface-exposed protein - Haemophilus influenzae C; Species: Haemophilus influenzae C; Species: Haemophilus influenzae C; Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994 C; Accession: B4385 R; Barramamp, S. J; Leininger, E. Infect. Immun. 60, 1302-1313, 1992 A; Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable details pertussis. A; Reference number: A43855; MUID:92192797 A; Accession: B4385 A; Secture: preliminary A; Molecule type: DNA A; Residues: 1-1477 <-BAR> A; Residues: 1-1477 <-BAR> A; Residues: 1-1477 <-BAR> A; Note: sequence inconsistent with the nucleotide translation A; Note: sequence extracted from NCBI backbone (NCBIN:89237, NCBIP:89240) A; Note: sequence extracted from NCBI backbone (NCBIN:89237, Indels 137; Gaps 30; Matches 139; Conservative 93; Mismatches 230; Indels 152; Gaps 30;	OY 11 SALNAWVVVSELTRNHTKRASATVKTAVLATLLEATVOASANNEEQEEDLYLDPVLR 67
	Oy 544 GGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNS 577	Query Match  Dest Local Similarity 23.6%; Score 228.5; DB 2; Length 1091;  Dest Local Similarity 23.6%; Pred. No. 0.0005;  Matches 147; Conservative 69; Mismatches 203; Indels 203; Gaps 36;  QY I MNEILRIIMNSALNAWWVYSELTRNHTRASATWTAVLATLLFATVQASANNEEQEEDL 60

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A; Molecule type: DNA
A; Residues: 464-2020 <MOS>
A; Residues: 464-2020 <MOS>
A; Coss-references: GB:D85081; NID:g3041754
A; Experimental source: strain K-12
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCB1 backbone (NCBIN:88089; NCBIP:88090)
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
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A;Residues: 1-839,'LDLPLYFQTSVIT' <BLA1>
A;Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1; PID:g17876
A;Experimental source: strain K-12, substrain MG1655
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A;Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g17876
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              near the replication terminus in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABC-type transport protein ydbA.2 - Escherichia coli
C;Species: Escherichia coli
C;Date: 19-Nov-1993 #sequence_revision 16-Oct-1998 #text_change 08-Oct-1999
C;Accession: C48399; D64891; H64891
E;Moszer, I.; Glaser, P.; Danchin, A.
Biochimie 73, 1361-1374, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1427
                         1138 LGNVSLTS-----SGRNIDINGSSAGTGDVYFTNVELNATAGNVSIYAETKTALS 1187
                                                                                                                                                                                                                                            1188 TSLNAVLSLGGNNSIKAQNGWLIGKAFNTTQGAGIGFRANSSLSVDGNIILKGETEGVGA 1247
                                                                                                                                                                                                                                                                                                                           | | | : : : | | | : : | | | | 10.248 TRKGIDFYGANTLNIIKGSQLSLLGENKGAQDTAGGNGISYTSLAKLTVNNNGSLKMEGR 1307
                                                                                                                                                                                                                                                                                                                                                                                                                      :| || || || || || || 1367 STGTGINFPSSNNTLVFNGDGDTLIKGSSVAGTGAAISGVVNNSTGPMTIEGISTDGAG 1367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ETVNINAGN----NIEITRNGKNIDIA-TSMTPQFSSVSLGA--GADAPT 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461 LSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAG 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 --IAQAIATAGL-VQAYLPGKSMMAIGGGTYRGEAGYAIGYSS-ISDGGNWIIKGTASGN
219 ---LNAGWNIKGV--KPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVK
                                                                                                274 IG--AKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTA--
                                                                                                                                                                                                 ------NGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITV-----
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A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                             ----SSGKVISGNVSPSKGKMD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown; translation not shown
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A;Ression: D64891
                                                                                                                                                                                                                                                                                            -----MYDVNVGDALNVNQLQNSGWNLDSKAVAG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Title: Multiple IS insertion sequences 1A, Reference number: A48399; MUID:92190338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: C48399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1547 GIG 1549
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C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C; Accession: AF0394
R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
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A;Residues: 1-1910 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:915981183; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1036 TKELKLTEDLSISGFN----KAEITAKDGRDLTIGNSNDGNSGAEAKTVTFN----NVK 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1236 --NGAEINATEGAATLTATGNTLTTEAGSS-----ITST-----KGQVDLLAQNGSIA 1281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNEEQEEDLYLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLK 111
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                                                                                                                                                                                                                                                                        328 TANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQN 387
                                                                                                                                                                       269 KTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGL-VTAKEVIDAVNKAGWRMKTT 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.3%; Score 219; DB 2; Length 1910;
20.5%; Pred. No. 0.0031;
ative 92; Mismatches 255; Indels 228; Gaps
                                                                                                                                                                                                                                                                                                                                                                        388 SGWNLDSKAVAGSSGKVISG--NVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFSSVSLGAGADAPTLSVDGDAL - - NVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVA
                                                                         209 KKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGK
                                                                                                                                                                                                                                                                                                                                                                                                  504 QNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable adhesin hmwA [imported] - Yersinia pestis (strain C092)
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1316 AKDAKLNGDASGDS 1329
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A; Status: preliminary
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A; Start codon: GTG

38; 84 KEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTE- 142 1 | | : ::|| |: 245 NGNNGKVIQDGDLDVSGGGGGGIDITGDSATVDNKGTMTVTDPESMGIQIDGDKAIVNNEG 304 EGLVTAKE-----VIDA----VNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 354 355 GTTATVSKDD-----QGNITVMYDVNVGDALNV----NQLQNSGWN--LDSK-----AVA 398 399 GSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSM-TPQFS----- 448 449 -SVSLGA-----GADAPTLSVDGDALNV---GSKKDNKPVRITNVA-----PGV---- 488 489 -KEGDVTNVAQLKGVAQN-LNNRIDNV-DGNARAGIAQAIATAGLV-----Q 532 700 GSDNNVTLDGKLTVVSDSEVTSRQSNLFDGSAE-----RTSGLVVIGDGNTVNMNGGL 752 151 TEKTLTIRDSVFTYTENADGTISLQDSNGRKATINLMQIDEANNTVALEGVSADGA---- 206 207 -----KTYVGKNHNGELVIT------GDNATVNNG------KTTVDGKDSTGTEI 244 143 ------KLSFSANGNKVNITSDT-----KG--------LNFAK 166 167 ETAGTNGDTTVHLNG-----IGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVL 219 220 NAGWNIKGVKPGTTASDNVDFVRTYDTVEF-LSADTKTTTVNVESKD------NG 267 359 GGGHGI-DITGDSATVDNKGTWTVTDPESIGIQVDGDQAVVNNEGESAITNGGTGTQING 417 268 KKTEVKIGAKTSVIKEKDGKLVTGKD-KGENG------SSTDEG 304 Gaps 33 TVKTAVLATLLFATVQ-----ASANNEEQEEDLY-LDPVLRTVAVLIVNSDKEGTGE 83 Ouery Match
7.2%; Score 216.5; DB 2; Length 2020;
Best Local Similarity 23.4%; Pred. No. 0.0044;
Matches 165; Conservative 78; Mismatches 238; Indels 225; 533 AYLPGKSMMAIGGGTYRGEACYAI-----GYSSISDGGNWIIKG 571 305 g 8 g qq ò g q δý qq g ò g Op ò g ò ò ò ò ò ŏ ŏ

Search completed: July 3, 2002, 08:12:25 Job time: 447 sec THIS PAGE BLANK (USPTO)

us-09-771-3\(\beta\)2-5.std.rsp

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GenCore version 4.5
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OM protein - protein search, using sw model

July 3, 2002, 08:30:02; Search time 48.34 Seconds (without alignments) 473.381 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-771-382-5 2999 1 MNEILRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 591

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		P33666 escherichia	P16466 proteus mir	-	P32051 escherichia					Q9kka3 r outer mem			Q9pjt6 chlamydia m					S	P38536 t amylopull	×	P34487 caenorhabdi	Q52657 rickettsia		_				-		Q9phw6 campylobact			P44969 haemophilus
SUMMARIES	Q	AG43_ECOLI		HLYA_PROMI	AIDA_ECOLI	YDEK_ECOLI	OMPB_RICRI	HLYA_SERMA	OMPA_RICRI	BIGA_SALTY	OMPB_RICCN	OMPB_RICTY	HXA2_HAEIN	Y741_CHLMU	HXA3_HAEIN	YPJA_ECOLI	OMPB_RICJA	WAPA_BACSU	SLAP_CAMFE	APU_THETU	ICEN_XANCT	YMJB_CAEEL	OMPA_RICCN	OMPB_RICPR	SLAP_CAUCR	SLAP_LACAC	ICEK_PSESX	120K_RICRI	FLIC_SHIFL	FLEY_CAUCR	FLID_CAMJE	ALYS_ENTFA	- 1	IGAO_HAEIN
	Length DB	1039	2003 1														1656 1												550 1			671 1		1694 1
d	Query Match Le	9.	7.2	•		•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•	•				•	•	•	•	٠	•	5.3	
	Score	28.	216.5	207.5	203.5	199	196	191.5	191	189.5	186.5	185	183.5	183	181	180.5	180	180	178.5	176	175.5	174	172.5	167		164.5	9	164.5		160.5	വ	159	159	159
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P45384 haemophilus P04949 escherichia	P50493 plasmodium 033479 pseudomonas P46949 saccharomyc	P80544 staphylococ P20676 saccharomyc	P06620 pseudomonas P38058 clostridium	Q06974 salmonella P56867 deinococcus	Q9zkw5 helicobacte
IGA2_HAEIN FLIC_ECOLI	PVDB_PLAKN ICEV_PSESX YG4A_YEAST	MRSP_STAAU NUP1_YEAST	ICEN_PSESY CBPA_CLOCL	FLIC_SALON HPI1_DEIRA	VACA_HELPJ
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55.3 13.3	22.3	5.2	5.2	5.2	5.1
159 158	157.5 157 156.5	156.5	155 155	154.5 154.5	154
34 35	36 37	3.0 4.0	412	4 4 4	45

## ALIGNMENTS

RESULT

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119 KONGINFIYSLKKDLIDLISVGIEKLSFSANGNKVNIISDIKGLNFAKETAGINGDIIVH 178
                                                                                                                                                                                                                                                                                                                                                                                                                         414 ALMLEKGSSFTLN------AGDTATDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    555 AIGYSSISDGGNWIIKGTASGN 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                        FEMS Microbiol. Lett. 149:115-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKI-- 118
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                                                 MEDLINE=97257509; PubMed=9103983;
Henderson I.R., Meehan M., Owen P.;
"Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTIGEN 43 ALPHA CHAIN.
ANTIGEN 43 BETRA CHAIN.
K -> N (IN STRAIN ML 308-225).
SL -> FF (IN STRAIN ML 308-225).
T -> K (IN STRAIN ML 308-225).
W -> L (IN STRAIN ML 308-225).
V -> F (IN STRAIN ML 308-225).
ATN -> STI (IN STRAIN ML 308-225).
ATN -> STI (IN STRAIN ML 308-225).
A -> T (IN STRAIN ML 308-225).
B -> V (IN STRAIN ML 308-225).
C -> V (IN STRAIN ML 308-225).
C -> V (IN STRAIN ML 308-225).
C -> Y (IN STRAIN ML 308-225).
C -> C (IN STRAIN ML 308-225).
                                                                                                                                                              -! - SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MNLIYNA (IN STRAIN ML 308-
                                                                                                                                                                              CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
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STRAIN ML 308-225).
STRAIN ML 308-225).
STRAIN ML 308-225).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 203;
                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.
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STRAIN ML 308-225)
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5170D647C8DEEBE0 CRC64;
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23.6%; Pred. No. 0.00031;
ve 69; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Complete proteome.
in the genome of Escherichia coli K-12.";
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A -> V (IN S
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QGT -> LGA (

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S -> I (IN S
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EMBL; D90838; BAA15825.1; ALT_INIT.
EMBL; D90839; BAA15832.1; ALT_INIT.
EMBL; U34429; AAB47869.1; --
ECOGENE; EG12686; flu.
Outer membrane; Signal; Complete prote
              Electrophoresis 18:1259-1313(1997).
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Best Local Similarity
Matches 147; Conserv
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585
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Alba H., Baba T., Fullta K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takedu J., Takenoti Y., Wada C., Yamanoto Y., Horinchi T.; Takenoto K., Takenoti Y., Wada C., Yamanoto Y., Horinchi T.; oorresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 TINGMIISTGLEYGPDNEANTGGQWVQDGGTANKTIVTSG--GLQ-RVNPGGSVSDTVIS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 NVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNG 434
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MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 TANTIVV-----YAGGDQTVHGHALDTILNGGYQYVHNGGTASDTV--VNSDGWQIVK
                                                                                                                                                                                                                                                                                                                                                  177 --VKPGTVATDTV--VNTGAEGGPDAENGDTGQFVRGDAVRTTIN----KNGRQIVRAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 NGGVAGNTTVN-QKGRL-QVDAGGTATNVTLKQGGALVTSTAATVT----GINRLGAFSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334 VEGKADNV-VLENGG-RLD-----VLTGHTATN-----TRVDDGGTLDV-RNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             435 KNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVT
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                                                                                       INGIGSTL----TDTLLNTG-----ATTNVTNDNVTDDEKKRAASVKDVLNAGWNI
                                                                                                                                                                                                                                                              226 KGVKPGTTASDNVDFVRT-----YDTVEFLSADTKTTVNVESKDNGKKTEVKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                 276 -AKTSVIKEKDGKLVTGKDKGENGSSTDE----GEGLV----TAKEVIDAVNKAGWRM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KTTTANGQTGQADKFETVTSGTNVTFASG----KGTTATVSKDDQG-NITVMYDV
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Mub B., Shao Y.;
Mub Complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                           136 AGG-GOSLOGRAVNTTLNGGEQWMHEGAIATGTVINDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDBA_ECOLI STANDARD; PRT; 2003 AA. P3366; P76087; P76088; P76085; P76859; O1-FEE-1994 (Rel. 28, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein ydba.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                   :| |:: : || :: : || : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | 
581 GSIGVLINGEGATVSNTGDVNVS-NEATGFSITTNSGKVSLAGSMQVGDFSTGVDLNGNN 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Uphoff T.S., Weich R.A.;
"Nucleotide sequencing of the Proteus mirabilis calcium-independent
"Nucleotide sequencing of the Proteus mirabilis calcium-independent
"Nucleotide sequencing of the Proteus sequence similarity with the
Serratia marcescens hemolysin genes (shla and shlB).";
J. Bacteriol. 172:1206-1216(1990).
-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 LTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVLRTVAVLIVNSDK--- 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
                                                                                                                                640 NSVTLAAKDLKVVGQKATGINVSGDANTVNITGNVLVDKDKTADNAAEYFFDPSVGINVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                 489 -KEGDVINVAQLKGVAQN-LNNRIDNV-DGNARAGIAQAIATAGLV-----
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W; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       449 -SVSLGA-----GADAPTLSVDGDALNV---GSKKDNKPVRITNVA--
                                                                                                                                                                                                                                                                                                                              533 AYLPGKSMMAIGGGTYRGEAGYAI-----GYSSISDGGNWIIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAY BE RESPONSIBLE FOR PORE FORMATION.
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22.3%; Pred. No. 0.0053;
iive 86; Mismatches 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1577 AA
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STRAIN-ISOLATE 477-12;
MEDLINE-90170827; PubMed-2407716;
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Best Local Similarity
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P16466;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 KEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKKDLTDLTSVGTE- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KLSFSANGNKVNITSDT----KG------------LNFAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETAGINGDITVHLNG-----IGSTLTDTLLNTGATINVTNDNVTDDEKKRAASVKDVL 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESTITNGGTGTQINGDDATANNNGKTTVDGKDSTGTEINGNNGKVIQD-----GDLDVS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 KGTMTVTDPESIGIQIDGDQAIVNNEG---ESTITNGGTG-----TQINGNDAT-ANNS 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSM-TPQFS----- 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 TEKTLTIRDSVFTYTENADGTISLQDSNGRKATINLWQIDEANNTVALEGVSADGA---- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TKWQYNHNGELVIT------GDNATVNNG------KTTVDGKDSTGTEI 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 TVKTAVLATLLFATVQ-----ASANNEEQEEDLY-LDPVLRTVAVLIVNSDKEGTGE 83
                                                                                                                                                                                                                     ESCHETICHIA COLI K-12.";
Biochimie 73:1361-1374(1991).
L- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGHGI-DITGDSATVDNKGTMTVTDPESIGIQVDGDQAVVNNEGESAITNGGTGTQING
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                                                                                                                                                                  Moszer I., Glaser P., Danchin A.;
*Multiple IS insertion sequences near the replication terminus in
Fecherichia coli K.12 ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 216.5; DB 1; Length 2003; 23.4%; Pred. No. 0.0026; tive 78; Mismatches 238; Indels 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220 NAGWNIKGVKPGTTASDNVDFVRTYDTVEF-LSADTKTTTVNVESKD----
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-> V (IN REF. 2).
B83A12C8B53220EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                           BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                          MEDLINE-92190338; PubMed-1665988;
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3:363-377(1996).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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KETDIDNRWFYSWKYDVTKEKEQIQQIGSQIDAKNNATLTATKGDVTLDAAKINAGNNLA 423
                                                                                                                                                                                                                                     KETAG-----GIGSTLTDTLL---NT 193
                                                                                                                                                                                                                                                                                                       531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 QTGQADKFETVTSGTNVTFASGKGTTATVS--KDDQGNITVMYDVNVGDALNVNQLQNSG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             767
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--- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                                                                                                                                               GATTNVTNDN-----VTDDEKKRAASVKDVLNAGWNIKG-----VKPGTTASDNVD
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Escherichia.
NCBL_TaxID=562;
                                                                                                    IKONGTNFTYSLKKDLTDLTSVG-TEKLSFSANGNKVNITS-----
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(Rel. 29, Last sequence update)
(Rel. 29, Last annotation update)
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MEDLINE=92326638; PubMed=1625582;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255 KTTTVNVESKDN----GKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVTA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356
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                                                                                                                                                                                                                                                                                                                                                                                                           61 TVSSGETQIVYSGRGNSNATVNSGGTQIVNNGGKTTATTVNSSGSQNVGTSGATISTIVN 120
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                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                               52 NNEEQEEDLYL-----DPVLRTVAVLIVN-------SDKEGT-GEKEKVEEN 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 TATVSKDDQGNITVMYD---VNVGD-ALNVNQLQNSGWNL------DSKAVAGSSG--K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNEILRIIWNSALNAWVVVSELTRNH-----TKRASATVKTA--VLATLLFATVQASA
                                                                                                                                                                                                                                                                                                                                        SDWAVYFNEKGVLTAREIT-----LKAGDNLKIKQNGTNFTYSLK-KDLTDLTSVGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 KEVIDAVNKAGWRMKTTTANG-----QTGQADKFETVTSGTNVTFASG------KGT
                                                                                                                                                                                                                                                                                    Indels 171;
                                                                                                                                                                                                                                                       Length 1286;
                                                                                                                                                                                            1286
.; 132271 MW; B2A00F72AC05FB34 CRC64;
                                                                                                                                                                                                                                                                                    92; Mismatches 274;
                                                                                                                                                                                                                                                       DB 1;
                                                                                                                          Cell adhesion; Signal; Outer membrane; Plasmid. SIGNAL
                                                                                                                                                                                                                                                     Ouery Match 6.8%; Score 203.5; DB Best Local Similarity 21.4%; Pred. No. 0.0065,
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                                                                                                              EMBL; X65022; CAA46156.1; -.
                                                                                                                                                                                                                                                                                      146; Conservative
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 595-1325 FROM N.A..
MEDLINE-94100243; PubMed-8274505;
Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
"An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochim. Biophys. Acta 1153:345-347(1993).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                    STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley W., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential).
SIMILARITY: TO E.COLI YFAL.
SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISP42 AND MOM38.
CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-ACYL DIGLYCERIDE (POTENTIAL)
N -> K (IN REF. 3).
M -> S (IN REF. 3).
W, 26A3A066FA19AD7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL LIPOPROTEIN YDEK
                                                                                                                                                                                                                                                Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S34315; S34315.
EcoGene; EG11780; YGKR.
PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
Hypothetical protein; Membrane; Lipoprotein; Signal;
01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein ydeK precursor (ORFT).
YDEK OR ORFT OR B1510.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                          MEDLINE=97251357; PubMed=9097039;
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MW
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1325 AA;
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                                                                                                                                                       SEQUENCE FROM N.A.
                                                                              Escherichia coli
                                                                                                                         NCBI_TaxID=562;
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CONFLICT
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MOM38.
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34;
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                                                                                                                                                                                                                                                                                                        139 VGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGA--- 195
                                                                                                                                                                                                                                                                                                                                         -----KGHVDGGYLRLGSSTGGVG------TVNVEGEDSVLTTELFEIGSYGT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 ----VVVEKGGEWLIKNNDSSIEFQIGNQGTGEATIREGGLVTAENTIIGGNATGIGTLN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               507 SGIVNVSNGATLNSTGYGFIGGNASGKGIVNISTDSLWNLKTSSTNAOLLQVGVLGTGEL 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IATAGLVQA-----YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI 568
                                                                                                                                                                                       61 GASLEVDNDQITNIDTDVAYDAYLVGWYGTGVLNILAGGNASLTTITTSVIGANEDSEGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 TITANGQIGQADKFETV-ISGINVIFASGKG-----ITAIVSKDDQGNIIVMYDVNVGD 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 ALNVN------QLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE-----TVNI 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAGNNIEITRNGK----NIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKP 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GTGEAFRYIYIGDAGDGELNVSSEGKVDSGIITAGMKETGTGNITVKDKNSVIT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 NLGTNLGYDGHGEMNISNQGLVVSNGGSSLGYGETGVGNVSITTGGMWEVNKNVYTTIGV 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          567 NITTGGIVKARDTQIALNDKSKGDVRVDGQNSLLETFNMYVGTSG--TGTLTLTNNGTLN 624
                                       Gaps
                                                                         1 MNEILRIIWNSALNAWVVVSELTR-----NHTKRASATVKTA--VLATLLFATVQAS 50
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                VN----VLGGTWRLY-------DSGNNARPLNVGQSGTG-TLNIKQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----VIDAVNKAGWRMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         281 VQDQDSVITVRRLYNGYFGNGTVNISNNGLINNKEYSLVGVQDGSHGVVNVTDKGHWNFL
                                                                                                                                                                                                                                                                                                                                                                                 -TTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 VRITNVAPGVK-----EGDVTNVAQLKGVAQNLNNRIDNV-DGNARAGIAQA----
DB 1; Length 1325;
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=783;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.011;
; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1654 AA
                                                                                                                                                    --LYLDPVLR--
6.6%; Score 199;
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                                   91;
                   21.0%;
                                     Conservative
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                   Similarity
                                                                                                                                                    51 ANNEEQEED-
                 Local Simi
hes 158;
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Q53047;
 Query Match
                                     Matches
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Length 1608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REQUIRES SHIB FUNCTION.
SUBCELLULAR LOCATION: Outer membrane.
SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.4%; Score 191.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                   439 IATSMTPQFSSVSLGAGADAPTLSVDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol. 170:3177-3188(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88257037; PubMed=3290200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165078 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      HLYA_SERMA STANDARD; F P15320; 01-APR-1990 (Rel. 14, Last sequol-NoV-1990 (Rel. 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M22618; AAA50323.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1608
                                                                         SPSKGKM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1608 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A28182; A28182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                   FGASA 585
                                                                                                                                                                                                                                                                                                                                                 762 FNTVA 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                      A S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 LLLNTANNLAVTVSEDTTLGFITNVVHNAHSFNLTLNAG---KTLTITGQGVTNAQAAAT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 NEEQEEDLYLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNAQNVVVQFNN-----GAAIDNNDLKGVG----RIDFGAPASTLVFNLANPTTQKAPLIL 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDNLKIKQNGTNFTYSLKKDLTDLT--SVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GGTTINFTGTDGTGRLVLLSKHAA--ATNFNITG------SGGTLKGVIE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQSAN---ATGOVNFRHIVDVGADGTTAFKTAASKVTITQDSNFGNTDFG-NLAAQIKVP 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|:
413 NAITLTGNFTGDASNPGNTAG--VITFDANGTLESASADANVAVTNNITAIEASGAGVVQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 IIWNSALNAWVVVSELTR------NHTKRASATVKTAVLATLLFATVQASAN 52
                                                                                                                                                                                          Gilmore R.D. Jr., Josten N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encoding the 120 kb surface-exposed protein of Rickettsia rickettsii.";
Mol. Microbiol. 3:1579-1586(1989).
-!- FUNCTION: THE 120 kba SURRACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A LAYER WITH HEXAGONAL SYMMETRY.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                      Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor."; Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTASDNVDFVRTYDTVEFLSADTKTTTVN------VESKDNGKKTEV--KIGAKTSV
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; Mismatches 282; Indels 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 KDA SURFACE-EXPOSED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.5%; Score 196; DB 1; Length 1654; 22.3%; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D7AB70FB7087F618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 KDA BETA PEPTIDE.
POLY-THR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                               STRAIN=R;
MEDLINE-90136087; PubMed=2515418;
                                          MEDLINE=92167802; PubMed=1724278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
Antigen; S-layer; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168184 MW;
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SEQUENCE OF 279-1654 FROM N.A.
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1654 AA;
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              FROM N.A.
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Matches 162;
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SEQUENCE
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                                                                                                                                                       438
                                                                                                                                                                                                                                       587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           706 FGSKGVNVDTVLNVGEGVNL----YATNITTTDANVGSFVFNAGGTNIVSGTVGGQQGNK 761
----TATVSKDDQGNITVMYDVNVGDALN--VNQLQNSGWNLDSKAVAGSSGKVISGNV 409
                                                                                                                                                                                                                                                                                                                            -- DALNVGSKK--- DNKPVRITN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poole K., Schiebel E., Braun V.; "Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                              -----DETVNINA-GNNIEITRNGKNI----D
                                                                                                                                                                                                                                       GNAGGAAALQRITLANDAKKTLTLGGANIIGAGGGTIDLQANGGTIKLTSTQNNIVVDFD
                                                                                                                                                                                                                                                                                                                                                                                                        588 LAIA-TDQTGVVDASSLTNAQTLTINGKIGTIGANNKTLGQFNIGSSKTVLSNGNVAINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            484 VAPGVKEGDV-----TNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPGK----SMMAIGGGTYRGEAGYA-----IGYSSISDGGNWIIKGTASGNSRGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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W; D669B476FE7DAD51 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NV-----GNTNALATVNVGAGL--LQVQGGVVKANTINLTDDNASAVTFTNPVVVTGAIDN 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 NEKGVLTAREITLKAGDNLKIKQNGTNFTYSLKK---DLTDLTSVGTEKLSFSAN----G 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820 GAVIKATTTKLTNAASVLTLTNANAVLTGAVDNTTGGDNVGVLNLNGALSQVTGDIGNTN 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GDT -- TVHLNGIGSTLTDTLLNT- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 TVNINAG-----NNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDAL--NVG 471
                          Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.; "A protective protein antigen of Rickettsia rickettsii has tandemly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     880 SLATISVGAGTATLGGAVIKATTTKLTN----AASVLTLTNANAVLTGAIDNTTGGDNV
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                                                                                                                              ΒY
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                                                                                                       -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
-1- SUBCELJULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED S-LAYER WITH HEXAGONAL SYMMETRY.
-1- PTM: GLYCOSYLATED (PROBABLE).
-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 2249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-layer; Glycoprotein.
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W; A9D6646C089DF087 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.4%; Score 191; DB 1
24.4%; Pred. No. 0.051;
ive 56; Mismatches 2
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A (TYPE I).
C (TYPE II).
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M (TYPE II).
                                                                    repeated, near-identical sequences.";
Infect. Immun. 58:2760-2769(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antigen; Repeat; Signal; Cell wall;
                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
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les 142; Conserv
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                                                                                                                                            ---NSDWAVYFNEKGVLTAREITLKAGDNLKIKQNG 122
                                                                                                                                                                                                                       123 TNFTYSLKKDLTDLTSVGTEKLS------FSANGNKVNITSDTKGLNFAKET 168
                                                                                                                                                                                                                                                                                                                                               618
                                                                                                                                                                                                                                                                                                                                                                                  GWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKD-NGKKT----EVKIGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                673 KTGNINVK------AAERQONIDEQKTALTVNGYAKEAGDKOYRAGLRIEHTRDSEK 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KTSVIKEKDGKLVTGKDKGENGSSTDEGEGLVT --- AKEVIDAVNKAGWRM ---- K 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  784 TKIGGGFYYTGGIDKLGSGVEAGYENNKTQAQSSKAITSGSDVKGNLT----INARDKLT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           889 VTRPVERAVGKAAKLDATGVINDIGGIGAPNVGLDIGAQGGSSEKRSSSSQAVVSSVQAG 948
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                                                                                                                                                                                                                                                                                                        169 AGTNGDTTVHLNG-IGSTLTDTLL--NTGATTNVTNDNVTDDEKKRAASVKDVLNA---- 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --- TVSKDDQGNITVMYDVNVGDALN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 SMTPQFSSVSLGA------GADAPTLSVDGDALNVGSKK--DNKPVRITNVAPG 487
                               Gaps
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16-CCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa antigen) (Cell surface
antigen) (rOmpA) (rOmp A).
                                                                                                                                                                                                                                                  : | | : : : | | | | 506 VHAQRDLTIDADNQIQYGVQKTANAKAVRDDKTSWGGIGGGDNKNN--SNRREISHASEL
                                                                RNHTKRASATVKTAVLATLLFATVQASANNEEQEEDLYLDPVLRTVAVLIVNSDKE----
                                                                                                     REQLOQAGSTVAASGSAKLI-----STQEDVKLLGANVSADRALSVKAARDVHLA
                                                                                                                                                                              446 GLVEKDKSSERGYORNHTSSLRTGRWSNSDESESLKASELRSEGELTLKAGRNVSTQGAK
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                                                                                                                                                                                                                                                                                                                                           564 --TSGG-TLRLNGQQGVTITGSKARGQKGGEVTATHGGLRID--NALSTTVDKIDARTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 VNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TANGQTGQADKFETVTSGTNVTFASGKGTTA----
                          223;
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Rickettsiaceae; Rickettsieae; Rickettsia.
0.033;
~hes 266; Indels
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      Pred. No. 0.03
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      21.5%;
      Best Local Similarity 21.5
Matches 157; Conservative
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P15921;
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-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 414 and 732.
1174 TVNVGAGITLQA----GSLAANNIDFGARSTLEFNGPLDGG------GKAIPYYFKGAIA 1224
                                                                  526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATRAIN-LT NOW NOT ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MEDLINE-21534948; PubMed-11677609;
MCCOLIAINA M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coli NADPH-sulfite reductase:
to overcome limiting siroheme
                                                                                                                                                         T----AGL-VQAYLPGKSMMA----SSIS
                                                                  SKKDN-KPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARA----GIAQAIA
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                                                                                                                                                                                                                                                                                                                                                                                                                  P25927; P25928; Q9XCQ3;
01-MAX-1992 (Rel. 22, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Putative surface-exposed virulence protein bigA precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Salmonella typhimurium rhs homolog.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                         DGGNWIIK------GTASGNSRGH---FGASASVG 588
                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1953 AA
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"High-level expression of Escherichia
requirement for a cloned cysG plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008859; AAL22340.1; -. EMBL; M64606; AAA27042.1; ALT_FRAME. EMBL; M64606; AAA27043.1; ALT_FRAME. PIR; C39200; C39200. PIR; D39200; D39200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91100301; PubMed=1987123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610 ADSVGFVVAGEKNTFKNKGDIDVSLNGTGALVS-GDMSQVTLDGDINV---VSVQDSEGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 FSSATGVSVSGDSNAVDITGNVNISADYGQDDLAAGAPPLTGVVVGGNGNTVTLNGALNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVAQLKGVAQNLNNRIDNVDGNARAG----IAQAIATAGLV------QAYLP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         280 VIKEKDGKLVTGKDKGENGSSTDEGEGLVT--AKEVI--DAVNKAGWRMKTTTANGQTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 GWILDSKAVAGSSGKV-ISGNVSPS------KGKMDETVNINAGNNIEITRNGK-NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --- DIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVRITNVAPGVKEGDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --GKSMMAIGGGTYRGEAG----YAI----GYSSISDGGNWIIKGTASGNSRGHFGA
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                                 POTENTIÀL.
PUTATIVE SURFACE-EXPOSED VIRULENCE
PROTEIN BIGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1953;
                                                                                                                                                                                                                                                                                                                                                      REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                      611B3F1C954D91AE CRC64;
                                                                                15 X 11 AA TANDEM REPEATS
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15 (INCOMPLETE).

D -> DRCDDDVTPPDD (IN REA -> RIN REF. 3).

D -> N (IN REF. 1).

QYLE -> ITLQ (IN REF. 1).

SA -> T (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.3%; Score 189.5; DE
23.1%; Pred. No. 0.051;
iive 64; Mismatches 1
                                                                                               (INCOMPLETE).
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               Signal; Complete
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                    Repeat;
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SG10437;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENDE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                     O9KKA3; O9KK98; O9XC45; 16-CT-2001 (Rel. 40, Created) 16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last sequence update) 16-CCT-2002 (Rel. 41, Last annotation update) Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Indian tick typhus, and Malish 7;
MEDLINE=20393643; PubMed=10939649;
Roux V., Raoult D.;
Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                            MEDLINE=21442074; PubMed=11557893; Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P -> A (IN STRAIN INDIAN TICK TYPHUS).

G -> S (IN STRAIN INDIAN TICK TYPHUS).

K -> N (IN STRAIN INDIAN TICK TYPHUS).

N -> A (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).
                                                                                                                                                                                                                                                                                                                                                           "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 KDA SÜRFACE-EXPOSED PROTEIN. 32 KDA BETA PEPTIDE.
                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen; S-layer; Cell wall; Complete proteome.
CHAIN 1334 120 KDA SURFACE-EX
CHAIN 1335 1655 32 KDA BETA PEPTID
                                          1655 AA
                                                                                                                                                                                                                        Rickettsiaceae; Rickettsieae; Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE008659; AAL03623.1; -. EMBL; AF123721; AAF34124.1; -. EMBL; AF123726; AAF34129.1; -. EMBL; AF149110; AAD39533.1; -. Interpro; IPR003858; rompA_rompB. Pfom; PF02708; rompA_rompB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 353-1655 FROM N.A.
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                                          STANDARD;
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                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=Malish 7;
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413
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          RESULT 10
OMPB_RICCN
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37;
I -> V (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

R -> L (IN STRAIN INDIAN TICK TYPHUS).

R -> GH (IN REF. 3).

E -> S (IN REF. 3).

G -> S (IN REF. 3).

G -> S (IN REF. 3).

H -> R (IN REF. 3).

A -> R (IN REF. 3).

A -> R (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 DLYLDPVLRTV--AVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 -----VVAQVNNGAAIDNNDLQGVGRIDCGAAAS--TLVFNLANP-TTQKAPLILGDNA 204
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                                                                                                                                                                                                                                                                                                                                                                                                              58
                                                                                                                                                                                                                                                                                                                                                                                                              10 NSALNAWVVVSELT------RNHTKRASATVKTAVLATLLFATVQASANNEEQEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 KIKQNGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 VI-VNGANGTLNVYNGFIKVSS-----KSF-ATVNVINI-GDGQGIMFNTDADNVNTLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 --GDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257 QANGATITFNGTDGTGRLVLLSKNAA--ATDFNVTG------SLGGNLKGI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GANAAVIGTNNG---A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TANGQTGQADKF-----ETVTSGTNVT-FASGKGTTA-TVSKDDQGNI-TVM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 NTANNLDVTVREDTTLGFITNVVNNANHFNLMLNAGKTLTITGQGITNVQAAATKNANN-
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                                                                                                                                                                                                                                                                                                         Length 1655;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                    6.2%; Score 186.5; DB 1; ·21.7%; Pred. No. 0.059; tive 78; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1645 AA.
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                                                                                                                                                                                                                           AA; 168342
                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 21.7%
Matches 162; Conservative
     959
988
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kba surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(Tomp B) [Contains: 120 kba surface-exposed protein (Surface protein antigen) (120 kba outer membrane protein ompB); 32 kba beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92104668; PUDMM-1729180;
Hackstadt T., Messer R., Cleplak W., Peacock M.G.;
Furidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettsiae: identification of an avirulent
mutant deficient in processing.";
Infect. Immun. 60:159-165(1992).
-i. FUNCTION: THE 120 kba SURRACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIL
VIRULENCE FACTOR AND/OR IMMONOGEN DUBING INFECTION.
-i. FUNCTION: THE 32 kba BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-i. FUNCTION: THE 32 kba BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-i. SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
                                                                                                                                                                                                                                                         MEDLINE-94040787; PubMed-8224886; Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.; Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.; "Cloning and Sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi."; Gene 133:129-133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92114896; PubMed-1370573;
Ching W.M., Carl M., Dasch G.A.;
"Mapping of monoclonal antibody binding sites on CNBr fragments of
the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
MEMBRANE ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-LAYER WITH HEXAGONAL SYMMETRY.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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-> S (IN REF. 2).
0CB5641C7EB185EE CRC64;
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V -> I (IN REF.
G -> A (IN REF.
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Pred. No. 0.069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION OF CLEAVAGE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunol. 29:95-105(1992).
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                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=WILMINGTON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigen; S-layer;
                                                                                                                                                                                                                                              STRAIN=WILMINGTON;
                                                                                                                              Rickettsia typhi.
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                                   99 TLAVIINENTILGEVINVIKOGNFFNFIIGAGKSLTIITGHGITAQQAATIKSAQNVVSKV 158
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                                                                          ---LTAREITLKAGDNLKIKQNGTNFTYSLK
                                                                                                                  159 NAGAAINDNDLSGVGSIDFTAAPSVLEFNLINPTTQEAPLTLGDNAKI-VNGANGILNIT
                                                                                                                                                          131 K---DLTDLTSVGTEKLSFSAN-GNKVNITSD-TKGLNFAKETAGTNGDTTVHLNGIGST
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                                                                                                                                                                                                                                                                                                                           ----SDN-----VDFVRTYDTVEFLSADTKTTTVNVESKD-----NGKKT---
                                                                                                                                                                                                                                             186 LTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGV-KPGTTA-----
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MEDLINE=95115556; Pubmed=7815944;
COPE L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
Mueller Eberhard U., Hansen E.J.;
"The 100 kDa haem:haemopexin-binding protein of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 HIG----KGVNLYANNITTTDANVGSLHFRSGGTSIVSGTVGG 758
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TGEKEKVEE-
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01-NoV-1995 (Rel. 32, Last sequence update)
01-CCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin-binding protein precursor (Hem
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STRAIN=DL42 / SEROTYPE B;
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Mol. Microbiol. 13:863-873(1994).
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                                                                              90 NSDWAVYFNE-KGV----
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68 TVAV-----
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                         VE-----GOTN 551
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                                 VAPGVKEGDVTNVAQLKGVAQNLNNRIDNV---DGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MOPN / Nigg;
MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
Nhite O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass &
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Owinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg &
Elsen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 28:1397-1406(2000).
-!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CT456/TC0741
FAMILY.
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NCBI_TaxID=83560;
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  -----NIDIATSMTPQFSSVSLGAGADAPTLSVDGDALN--
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16-0CT-2001 (Rel. 40, Last sequ
16-0CT-2001 (Rel. 40, Last anno
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                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                        Cope L.D., Yogev R., Mueller-Eberhard U., Hansen E.J.;
A gene cluster involved in the utilization of both free heme and heme:hemopexin by Haemophilus influenzae type b.";
J. Bacteriol. 177:264-2653(1995).
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6 X 6 AA APPROXIMATE REPEATS.
1-1.
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1-5.
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4 X 6 AA APPROXIMATE TANDEM REPEATS.
2-2.
2-3.
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928 AA;
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                                                                                                                                                                                                                                                                             655 TVYPGENGGSTEGPL--PANQNLGNVIHDVEQNGAAQE--TIITPGDTESTDTSSSVNAN 710
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16-OCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
158 DTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGAT-TNVTNDNVTDDEKKRAASVK
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                                                 DVLNAGWNIKGVKPGT-TASDNVDFVRTYDTVEFLSADTKT---TTVNVESKDNGKKTEV
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Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The 100 kDa haem:haemopexin-binding protein of Haemophilus
                GDDGISFSNETIGSEPFATPPSSPSQTPVINVNVVGGTNVNIGDTNVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-NTHI N182;
MEDLINE=95115556; PubMed=7815944;
Cope L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
Mueller-Eberhard U., Hansen E.J.;
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Mol. Microbiol. 13:863~873(1994).
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                                                                                                      273 KIGAKTSVIKEKDG----KLVTGKDK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       500 KGVAQNLNNRIDNV---DGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAI
                                                                                                                                                                                                                                                                                                                             6 AA APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 212; Indels 124;
                                                                HEME/HEMOPEXIN-BINDING PROTEIN.

3 X 5 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%; Score 181; DB 1; Length 917; 21.6%; Pred. No. 0.054;
                                                                                                                                                                         APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                          ;-2.
7FF39BB8C046539D CRC64;
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                                              SIMILARITY
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P52143; P76610; P77017; P77019
01-OCT-1996 (Rel. 34, Created)
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EMBL; U08349; AAA74139.1;
                          Repeat.
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Best Local Similarity
Matches 117; Conserv
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917 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                   137 TSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGDTTVHLNG------IGST 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 INGGTQNINNYGIATGTNINSGTQNIK-----SGGKADTTIISSGSRQVVEKDGTAIGSN 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 FVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGS 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 NHTKRASATVKTAVLATLL-----FATVQASANNEEQEEDLYLDPVLRTVAVLIVNS 76
                                                                                                                                                                                                                                                                                                                                                          Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
                                                                                                                                                                                              Perna N.T., Burland V.,
                                                                                                                                                                          MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322 NVTQHDGAILKTNTNGTTVSGTNSEGAFSIHNHVADNVLLENGGHLD----
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Pred. No. 0.11;
2; Mismatches 277; Indels
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Hypothetical protein; Outer membrane; Complete proteome.
SEQUENCE 1569 AA; 162774 MW; 0D006A9A32154596 CRC64;
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical outer membrane protein ypjA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U36840; AAA79815.1; ALT_SEQ. EMBL; AE000350; AAC75695.1; --
EMBL; D90889; BAA16514.1; ALT_INIT
EMBL; D90890; BAA16518.1; ALT_INIT
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MEDLINE=97349980; PubMed=9205837;
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Matches 117; Conservative 102;
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                                                                                                                                              SEQUENCE FROM N.A. STRAIN=K12 / MG1655;
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                 Escherichia coli.
                                                                                                              NCBI_TaxID=562;
                                 Hypothetical YPJA OR B2647
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Search completed: July 3, 2002, 08:30:09 Job time: 1180 sec

09jps8 neisseria m 09jps7 neisseria m 09jqy2 neisseria m 09jqy0 neisseria m 09jph0 neisseria m 09jph0 neisseria m 09jps7 neisseria m 09jps4 neisseria m 09jps4 neisseria m 09jps4 neisseria m 09jqw4 neisseria m 09jqs4 neisseria m 09jps7 neisseria m 09jps8 neisseria m 09jps8 neisseria m 09jps8 neisseria m 09jps8 salmonella 09jc4 saturella 09jc4 rhizobium m 09gh03 xylella fas 09jc4 staphylococ 09ge20 rhizobium lus 09jc4 staphylococ 09ge20 rhizobium lus 09fda0 xanthomonas 09fda0 xanthomonas 09fda0 xanthomonas 09lc7 escherichia

Perfect score:

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Sequence:

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Run on:

Scoring table:

Searched:

Database

Q9a150 shigella fl Q48028 haemophilus Q916t8 escherichia

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STRAIN-EG329;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157606; AAK68867.1; -.
SEQUENCE 591 AA; 62048 MW; CODC600798859C65 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNEILRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 2999; DB 2;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 591; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       591 AA
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09F3X6
09F2D8
09F2D8
09F3X5
09F3X5
098HJ2
098HJ2
                                 Q93QY2
Q9JPH0
Q9JPS5
Q9JPI0
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Q48028
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Q9L6T7
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                                                                     NHHA OUTER MEMBRANE PROTEIN.
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                                                                                                                                                                                                                2999
1 MNEILRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 591
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                                   Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                          562222 seqs, 172994929 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      protein search, using sw model
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Q9JPS7
Q9AQF0
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
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Q93QY5 Q9JPR8 Q9JPS9

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2984 29880 29880 2866.5 2752.5 2739.5 2728.5 2728.5 2719.5 2719.5 2706.5 2706.5 2597.5

Score

Result . 9

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SEQUENCE FROM N.A. SPECIES=N.meningitidis; STRAIN=PMC21;
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Best Local S:
Matches 588,
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SEQUENCE FROM N.A.

STAIN=WC58 / SENGGROUP B, BZ169, BZ83, AND H44/76;

MEDLINE-20175756; Pubmed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,

Comanducci M., Jennings G.T., Manetti R., Marachetti E., Mora M., Nuti S

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
       GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                              VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                              241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup
Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLRel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision;
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MEDLINE=20175755; PubMed=10710307;
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Science 287:1816-1820(2000)
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NCBI_TaxID=487, 491;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel of membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ARE226375, ARF42524.1;
EMBL; ARE226375, ARF42516.1;
EMBL; ARE26377, ARF42516.1;
EMBL; ARE26377, ARF42519.1;
EMBL; ARE26371, ARF42519.1;
EMBL; ARE26371, ARF4253.1;
EMBL; ARE26371, ARF4253.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                             Score 2984; DB 16;
Pred. No. 2.9e-118;
1; Mismatches 2;
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EMBL; AF157611; AAK
TIGR; NMB0992; -
Complete proteome.
SEQUENCE 591 AA;
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a gene encoding a novel outer
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Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                              Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jenn "Identification and characterisation of a gene encoding membrane protein of Neisseria meningitidis."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AFL5375; AAK09243.1; SEQUENCE 592 AA; 62290 MW; 168986A9738IEFC5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                Query Match 98.4%; Score 2952.5; DB 2; Best Local Similarity 98.5%; Pred. No. 6.1e-117; Matches 583; Conservative 4; Mismatches 4;
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Bacteria; Proteobacteri
                                                                 SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=487;
                                  NCBI_TaxID=487;
                                                                                  STRAIN=MC58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9JPS3;
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                                                                             Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Hood D.W., Hoffies A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; Maningococcus by Whole-Genome Sequencing. Scrogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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                                                                                                                                                                                                                                                                                                                   Length 591;
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SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                 Score 2980; DB 2;
Pred. No. 4.3e-118;
2; Mismatches 2;
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                                                              MEDLINE-20175756; PubMed-10710308;
                                                                                                                                                                                                                                                                                                                 Query Match 99.4%;
Best Local Similarity 99.3%;
Matches 587; Conservative
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
OUTER MEMBRANE PROTEIN.
                                FROM N.A.
 NCBI_TaxID=487;
                                                  STRAIN-B2147;
                                SEQUENCE
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Q9AQFO;
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RESULT **09AQF0** 

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Length 600;

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117 KIKQ-----NGTNFTYSLKKDLFDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG 170
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                                                                                                                                                                                                                                                                                                                                                                                                                   Pizza M., Scarlato V., Masignani V., Giullani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Sanders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R., "Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 KIKQNTDENTNASSFTYSLKKELTDLTSVGTEKLSFGANGNKVNITSDTKGLNFAKETAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           531 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQ
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                                                                                                                                                                                                                                                                                                                                                            25; Indels
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SEQUENCE 600 AA; 62762 MW; 36256963E059BCD1 CRC64;
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Last sequence update)
                                                                                                                                                                                                                                                                                                                        91.8%; Score 2752.5; DB 2
91.3%; Pred. No. 1.6e-108;
ive 16; Mismatches 25;
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                                                                                                                                                                                                             Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
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                                                   MEDLINE=20175756; PubMed=10710308;
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.3
Matches 549; Conservative
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                 SEQUENCE FROM N.A.
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01-DEC-2001
01-DEC-2001
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=487;
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Science 287:1816-1820(2000).

EMBL; AF226378: AAF422377.1: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSKKDNKPV
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                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                      Length 590;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                    Score 2866.5; DB 2;
Pred. No. 2.5e-113;
5; Mismatches 13;
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               MEDLINE=20175756; PubMed=10710308;
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96.5%;
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zori Broeker M., Huddt E., Knapp B., Blair E., Mason T., Tettellin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R., "Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                    Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AF226379; AAF4252B.1; -
EMBL; AF226379; AAF4252B.1; -
                                             MEDLINE=20175756; PubMed=10710308;
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OUTER MEMBRANE PROTEIN GNA992.
GNA992.
Bacteria, Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                             Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                                         Jennings M.P.
                                                                                        STRAIN-EG327;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R:, Jenning T. Gentification and characterization of a gene encoding in membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157605; AAK68866.1; -.
SEQUENCE 594 AA: 62297 WW; 9DDD48B04B3ABEA2 CRC64;
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; Pred. No. 5.5e-108;
15; Mismatches 23;
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                                                         NCBI_TaxID=487;
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   2; Length 594;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
; Score 2732.5; DB 2;
; Pred. No. 1.1e-107;
14; Mismatches 25;
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Matches 548; Conservative 14
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                                                                                                                                                                                                                                                         MNEILRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
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           subdivision; Neisseriaceae;
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; Pred. No. 1.6e-107;
14; Mismatches 26;
                                                                                                                                               Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
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STRAIN-NG3/88, AND BZ232;
MEDLINE-20175756; Pubmed-10710308;
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Neisseria meningitidis.
Bacteria; Proteobacteria;
NCBI_TaxID=487;
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STRAIN=BZ198, AND 297-0;
STRAIN=BZ198, AND 297-0;
MEDILINE=201755; PubMed=10710308;
MEDILINE=20175756; PubMed=10710308;
A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
A Ratti G., Santini E., Kanep B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.;
A Moxon E.R., Grandi G., Rappuoli R.;
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
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                                                            Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 594;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.7%; Score 2721.5; DB 2; Length 91.6%; Pred. No. 3.1e-107; ive 12; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62361 MW; 436BDDED68263C5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 AA;
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Best Local Similarity
Matches 548; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=487;
                                          GNA992 OR NHHA
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117 NINENTNENTNESSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG 176
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Caleotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S Ratti G., Santini L., Savino S., Scarselli M., Storni,E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.K., Granoff G., Rappuoli R., Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 INGDITVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNEILRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 477 VGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNALAGIAQAIATAG
                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63A6A3BD7F0F2EE3 CRC64;
                                                                                                                                                                                                                                                            01-0c7-2000 (TrEMBLrel. 15, Created)
01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
101-MR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN (BNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 90.2%; Score 2706.5; DB 2; Best Local Similarity 90.4%; Pred. No. 1.3e-106; Matches 544; Conservative 14; Mismatches 29;
                                                                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20175756; PubMed=10710308;
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SEQUENCE 598 AA; 6276
                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=487;
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QW 598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296
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                                                                                                                                                                                                                             Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487.
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Science 287:1816-1820(2000).

SEQUENCE 598 AA, 62718 MW; 9095F8B3IAD7C76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        534 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.7%; Score 2719.5; DB 2; Length 598; 91.0%; Pred. No. 3.8e-107; ive 12; Mismatches 27; Indels 15;
                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                       598 AA
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                 STRAIN=NGH36;
MEDLINE-20175756; PubMed-10710308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548; Conservative
                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
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Matches 54
                                                                                                                      Q9JPR9
                                                                                                                                        O9JPR9
                                                                                                                                                                                                                           GNA992
                                                                                   RESULT 11
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177 TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 236
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                                                                                                                                                                                                                                                                                                                                                                              598
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hes 544; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis
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01-DEC-2001 (
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Q93QY5;
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                                                                                                                                                                                                                                                                                                                                                            PIZZA M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Capecti E., Marchi C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Kappp B., Blair E., Mason T., Tettelin H., Moxon E.R., Grandi G., Rappuoli R.; Granoff D.M., Venter C., "Identification of Vaccine Candidates Against Serogroup B
           MNEILRIIMNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG
PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN
                                           VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                        LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
                                                                                                                                                                                                                                        Created)
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NCBL_TaxID=487;
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                                                                               GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel o
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 1.5e-106;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                      GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT
           VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
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                                           GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Identification and characterization of a gene encoding a novel c membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AR226383; AAR42532.1;
EMBL; AR157608; AAK68869.1;
SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
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Pred. No. 2.6e-105;
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT: *
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT: *
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/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
/SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
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AAY23739
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N. meningitidis PM
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A surface protein
BASB029 amino acid
N. meningitidis EG
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N. meningitidis EG
A surface protein
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22 AAB691:	AAB691	ABB526	AAB378	AAB238	AAB238	AAB238	AAB238	AAB	AARS		AAB	AAY	AARS	AAB						AAU06		2 AAU0617			AAU0	AAY23	AAU0	AAY23	2 AAU0617	AAY23	AAU061	AAY237	AAU061
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## ALIGNMENTS

RESULT AAY23741

AAY23741 standard; Protein;

591

B

AAY23741;

08-SEP-1999 (first entry)

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Neisseria meningitidis surface proteins useful for treating meningitidis infections
                              WPI; 1999-418754/35.
N-PSDB; AAX85793.
                                                                                                                                                                                                  A surface protein of Neisseria meningitidis
                                                      Jennings MP,
                                                                                             12-DEC-1997;
                                                                                                            14-DEC-1998;
                                                                                                                            24-JUN-1999.
                                                                                                                                           W09931132-A1
                                                                                                                                                           Neisseria meningitidis
                                                                                                                                                                                   Surface protein; surface glycoprotein; infection; vaccine;
                                                                    (UYQU ) USIS
                                                                                                                                                                          immunoreactive peptide.
                                                                    INNOVATION LTD QUEENSLAND.
                                                      Moxon ER,
                                                                                             97GB-0026398
                                                                                                            98WO-AU01031
                                                      Peak IRA;
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RESULT
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especial in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                              Z
                                                                                                            AAU06175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in human.
 Neisseria
                      Surface antigen NhhA; meningococcal disease; meningitis vaccine
                                                                   24-OCT-2001
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                                            meningitidis
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                                                                                                                                                                MAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 591
                                                                                                                                                                                                                                                               NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
                                                                                                                                                                                                                                                                                              YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
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                                                                                                                                                                                                                        ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                                                                                                                                                                    {\tt ninagnnieitrngknidiatsmtpqfssvslgagadaptlsvdgdalnvgskkdnkpvr}
                                                                                                                                                                                                                                                                                                                                                                                     VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
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                                                                                                                                                                                                            itnvapgvkegdvtnvaqlkgvaqnlnnridnvdgnaragiaqaiataglvqaylpgksm
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                                                                                                             standard;
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meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; ilarity 100.0%; Conservative
                                                                  (first entry)
                                         EG329 surface antigen NhhA polypeptide sequence
                                                                                                             Protein;
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                                                                                                             591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2999; DB 20;
Pred. No. 5.9e-169;
); Mismatches 0;
 EG329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              surface protein of Neiserria
ly 62 kDa. The N. meningitidi
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Query Match Best Local Matches

591;

Conservative

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Similarity

100.0%;

Score 2999; DB 22; Pred. No. 5.9e-169; Mismatches

Length

591; 0,

Gaps

0

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strains given in (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                 Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          preventing broad spectrum of Neisseria meningitidis
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Region
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treat
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                                        present invention.
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591 AA;
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14-JAN-1998;
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DB; AAX99124.
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                                     CHIRON
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                                                                                                                         meningitidis protein;
infection; treatment.
                                                                                                             meningitidis
                                                                                                                                            sequence
                        Masignani
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                                                98GB-0022143.
98GB-0000760.
98GB-0019015.
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AAY23746

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Protein;

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A surface

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of Neisseria meningitidis

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Matches 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New protein and its nucleotide sequence, useful in vaccines diagnostic compositions for treating and/or preventing Neis: meningitidis infections
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Pred. No. 4.5e
1; Mismatches
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No. 4.
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Query Match
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Matches 588;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-418754/35.
N-PSDB; AAX85798.
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                                                                          SKDDQGNITWMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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Pred. No. 4.5e-168;
1; Mismatches 2;
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                                          25-JAN-2000;
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237..591
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52..591
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230..23
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/mote= "Conserved
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claimed in claim 12"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain PMC21 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                  ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSM
                                                                                                             ninagnnieitrngknidiatsmtpqfssvslgagadaptlsvdgdalnvgskkdnkpvr
                                                                                                                           NINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPVR
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Serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and collapsetide sequences (AAX57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 particularly bacterial infections. The protein is useful in the diagnosis of screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Fig 2; 74pp; English.
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Query Match 91.3
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Pred. No. 1.2e-153;
5; Mismatches 23;
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                         polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the stimulation of the immune system of an organis
                                                                                                                                                                                                                          This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY57044 standard;
                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide from neisseria meningitidis useful treatment or prevention of bacterial infections in
                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAZ39864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASB029 amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                        Fig
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                                                                                                                                                                                                                                                                                                                                                         2; 74pp;
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                                                                                                                                                              meningitidis
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                                                                                                                                                                                                                                                                         KDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 533
                                                                                                                                                                                                                                                                                                                                                                                                         GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
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                                                                                                                                                                                                                                                                                                                                                                                             gttatvskddqgnitvmydvnvgdalnvnqlqnsgwnldskavagssgkvisgnvspskg
                                                                                                                                                                                                                                                                                                                                                                                                                                     gendsstdkgeglvtakevidavnkagwrmktttangqtgqadkfetvtsgtnvtfasgk
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                                                                                                                        meningitidis strain
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                                                                                                                                                                                  (first entry)
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                                                                                                                                          Nhha;
 /label= C2
/note= "Conserved
117..126
                                                            /note= "Conserved 51..104.
                                                                                                                                                              EG327
                               /note= "Variable
105..116
                                                                                /label=
                                                                                                   Location/Qualifiers
                                                   /label=
                                                                                                                                                                                                                          Protein;
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91.8%;
                                                                                                                                                              surface
                                                                                                                                          meningococcal disease; meningitis
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Pred. No. 1.2e-153;
5; Mismatches 23;
                                                                                                                       EG327
                                                                                                                                                              antigen NhhA polypeptide sequence
                                        region
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                                                                                                                                                                                                                     The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antiqen Nhha (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding whild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences (AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Fig 1; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                              New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-JAN-2000;
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              121
                                   58
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                                                                                                                                Local Similarity
les 549; Conserv
                                -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD
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DB; AAS09164.
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                                                                                                                                                                                                               invention.
                                                                                                                                Conservative
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213..23
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127..190
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232..23
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191..212
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/note= "Conserved
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239..594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . 238
                                                                                                                             91.3%; Score 2739.5; DB 22; 91.8%; Pred. No. 1.2e-153; tive 15; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Variable
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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also
                                                                                                                                                                                   (ISIS-)
                                                                                                                                     N-PSDB;
                                                                                                                                                                 Jennings
                                                                                                                                                                                                                                                                                                                                          A surface protein
                                                                                                                                                                                                                                                                                                                                                                                                    AAY23739
                                                                                       Claim 1;
                                                                                                         Neisseria meningitidis meningitidis infections
                                                                                                                                                                                                                12-DEC-1997;
                                                                                                                                                                                                                                   14-DEC-1998;
                                                                                                                                                                                                                                                                                           Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                              08-SEP-1999
                                                                                                                                                                                                                                                                                                             Surface protein; surface glycoprotein; immunoreactive peptide.
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DB; AAX85791.
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                                                                                                                   useful for
                                                                                                                  treating
                              humans.
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Best Local
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Region
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                                                                                                                                   meningitidis BZ198
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                                                                                                                                                                                                                                                                                           KDNKPYRITNYAPGYKEGDYTNYAQLKGYAQNLNNRIDNYDGNARAGIAQAIATAGLYQA 533
                                                                                                                                                                                                                                                                                                                                                                       GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ntnentndssftyslkkdltdltsveteklsfgangnkvnitsdtkglnfaketagtngd
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                                                                                                                                                                                                                                                                                                                                                            gttatvskddqgnitvkydvnvgdalnvnqlqnsgwnldskavagssgkvisgnvspskg
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                                                                                                                  antigen
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                                                                                                                                                       (first entry)
                                        /note=
51..104
                                                                                                                  NhhA;
/note= "Variable region
105..116
/label= C2
                                                          /label=
                                                                           Location/Qualifiers
                              /label=
                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoreactive peptides
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91.6%;
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                                                                                                                  disease;
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les 27;
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                                                                                                                                                                                                                          The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain BZ198 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                     New NhhA surface antigen polypeptides and polynucleotides from 
Neisseria meningitidis, useful in producing vaccines for treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001;
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                                                                                                                                 Local Similarity
mes 548; Conserv
                                                                                                                                                          Match
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                                                                                             MNEILRIIWNSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL
                                  YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120
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DB; AAS09169.
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nilarity 91.6%;
Conservative 1
NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD
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239..594
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213..2
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117..1;
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/note= "Variable
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Pred. No. 1.3e
12; Mismatches
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                                                                                                                                                                                 Claim 1; Page 108-110;
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surface glycoproteins, nucl a thermostable polymerase, the detection or diagnosis The N. meningitidis surface

ch is approximately 62 kDa. The N. meningitidis teins, nucleic acids, the primers and optionally olymerase, or antibodies are useful in a kit for diagnosis of N. meningitidis infection in humans

surface glycoproteins

ç humans meningitidis which

sequence represents a

surface protein of Neiserria

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       Key
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                                Neisseria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t or treat N. meningitidis infection in humans, especially form of vaccines. The proteins and antibodies can also it o identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                               meningitidis
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                                              NhhA;
                                                               H15
              Location/Qualifiers
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90.5%;
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                                              disease; meningitis vaccine
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Query Match Best Local S Matches 545

Local Similarity 90. hes 545; Conservative

90.2%;

Score 2706.5; Pred. No. 1e-1 l3; Mismatches

6.5; D 1e-151

BB 29; 22;

Length

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antiqen Nhha (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and prophylactic vaccines against a broader medicaments. The mutant proteins when used as a vaccine can effective immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.
                                                                                                                                                                                                                   New NhhA surface antigen polypeptides and polynucleotides Neisseria meningitidis, useful in producing vaccines for preventing broad spectrum of Neisseria meningitidis -
                                The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain H15 is 1 of 10 Nhha polypeptide sequence (AAU06171-AAU06180) from 10 different N. meningitidis strains given
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                                              INNOVATION LTD QUEENSLAND.
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                                 Moxon
                                                                   97GB-0026398
                                                                                98WO-AU01031
                                                                                                                                                       of Neisseria meningitidis.
                                                                                                                                                                                               Protein;
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                                  Peak
                                  IRA;
proteins useful for
                                                                                                                                           infection; vaccine;
treating
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Matches 544;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis infections
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                                       TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
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                                                                                            VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
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Result
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Perfect score:
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3: /cgn2_6/ptodata/2,
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US-09-377-155-17
US-09-669-974-15
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ALIGNMENTS

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; ORGANISM: Neisseria meningitidis US-09-377-155-11
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US-09-377-155-11
                                                                      SOFTWARE: Pa
SEQ ID NO 11
LENGTH: 591
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09377155 Patent No. 6197312
                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                     APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE AIFILE REFERENCE: 065064/0128
                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                TYPE: PRT
                                                                                                                 PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                               NOVEL SURFACE ANTIGEN
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Local Similarity
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                             VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                           VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 360
                                                                                                                                                                                                                                                                                                                100.0%; Score 2999; DB 4; ilarity 100.0%; Pred. No. 4.8e-224; Conservative 0; Mismatches 0;
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APPLICANT: PERK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
SOFTWARE: PATENTION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                     VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKDKGENGSS
                                                                                                                                                                                                                                                    GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
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                                                                                          GIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
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Pred. No. 4.8e-224;
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US-09-377-155-21
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TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
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SEQ ID NO 21
LENGTH: 591
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Best Local Similarity
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                              TDEGEGI.VTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV 360
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SKDDQGNITYMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
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Pred. No. 6.9e-223;
1; Mismatches 2;
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GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065964/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT EILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILLING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR FILLING DATE: 1998-12-14
PRIOR FILLING DATE: 1997-12-12
PRIOR FILLING DATE: 1997-12-12
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Best Local Similarity 99.5%;
Matches 588; Conservative 1
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LENGTH: 591
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Pred. No. 6.9e-223;
1; Mismatches 2;
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APPLICANT: MCNON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: D726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEO ID NOS: 33
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Best Local Similarity
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VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
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Pred. No. 1.9e-220;
4; Mismatches 4;
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GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/09/377,155
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GE 199-08-19
PRIOR APPLICATION NUMBER: GE 9726398.2
PRIOR FILING DATE: 1997-12-12
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US-09-669-974-2
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Best Local Similarity 98.5%;
Matches 583; Conservative
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                   VNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGDALNVGSKKDNKPV
                                                       VSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDET
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Pred. No. 1.9e-220;
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RESULT 7
US-09-377-155-9
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PRIOR APPLICATION NUMBER: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 97
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
COUNTMARE: Patentin Ver: 2.0
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SEQ ID NO 9
LENGTH: 594
TYPE: PRT
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Best Local Similarity
Matches 549; Conserv
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
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                                                                 GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
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91.8%; Pred. No. 5.7e-204;
tive 15; Mismatches 23;
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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SEQ ID NO 9
LENGTH: 594
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Best Local Similarity
Matches 549; Conserv
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Patent No. 6333173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Neisseria meningitidis -09-669-974-9
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NNKIYRIIWNSALNAWVAVSELTRNHTKRASATVATAVLATLLFATVQASTTD----DDDL
                                                                                                                                              KDNKPYRITNVAPGYKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA
                                        KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK
                                                                                          TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 234
                                                                                                                                                                                                                                                                                                           NTNENTNASSFTYSLKKDLTDLTSVGTEKLSFSANSNKVNITSDTKGLNFAKKTAETNGD
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Pred. No. 5.7e.
15; Mismatches
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es 23;
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Best Local Similarity
Matches 548; Conserv
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SOFTWARE: PatentIn Ve
SEQ ID NO 7
LENGTH: 594
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                                                                     KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALNVGSK 473
                                                                                                                                               ----- NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNGD
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                             DTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA
                                             KDNKPYRITNVAPGYKEGDYTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 533
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER: GB 9726398.2
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APPLICANT: PEAK, Ian Richard Ansell
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE;
FILE REFERENCE: 065064/0128
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Best Local Similarity
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                                                                                                                                                                                   GTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
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                                           DTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA
                                                                                                                                                                   GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
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                                                                                                        KMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSK
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Pred. No. 1.4e-202;
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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Patent No. 6197312
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
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61 YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120 1 MNEILRIIWNSALNAWYVVSBLTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL ||:|||||||||||||. LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS GKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTF GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP NTNENTNESSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG -----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN 90.2%; Score 2706.5; DB 4; 90.5%; Pred. No. 2.1e-201; bive 13; Mismatches 29; Indels Length 598; 15; 529 476 469 350 296 290 236 176 57 589 536 416 356 4.

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LENGTH: 598
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APPLICANT: PEAK, Ian Richard Anselm
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CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
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PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
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LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY
                                                                                                                         PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN
                                                                                                                                                                                     ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                                                                                                                   GKDKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
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                                                                            VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                                           PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                                                                     ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
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, Sequence 5, Application US/09377155
, Patent No. 6197312
, GENERAL INFORMATION:
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SOFTWARE: PatentIn Ve
SEQ ID NO 5
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
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                           VGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                  PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN
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90.4%; Pred. No. 2.50
tive 14; Mismatches
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GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR TILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: DS 9726398.2
PRIOR FILING DATE: 1997-12-12
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                                                                                                                                   ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
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                                                    PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                  ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
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PRIOR FILING DATE: 1997-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver. 2:
SEQ ID NO 15
LENGTH: 599
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, ERichard
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Sear Job	Db	Qy	рь	Qy	Ф
ch com time:	598	590	538	530	478
Search completed: Job time: 531 sec	598 QW 599	590 QW 591	LVQAYL	LVQAYL	 VGSKDA
: July			PGKSMM	PGKSMM	 NKPVRI
ω			AIGG	AIGG	TNVA
Search completed: July 3, 2002, 08:10:19 Job time: 531 sec			538 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 597	530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 589	1111
08:			AGYA	AGYA	 DVTN
10:19			IGYSS	IGYSS	VAQLK
			ISDGG	ISDGG	GVAQN
			NITWI	NIIWN	LNNRJ
			(GTAS	(GTAS	DUVDO
			GNSRG	SNSRG	SNARA
			HFGAS	HFGAS	GIAQA
			ASVGY	ASVGY	  IATAG
			597	589	537

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## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 3, 2002, 08:09:09; Search time 168.6 Seconds (without alignments) 394.622 Million cell updates/sec Run on:

US-09-771-382-6 3060 1 MNKIYRIIWNSALNAWVAVS.....TASGNSRGHFGASASVGYQW 599 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 segs, 111073796 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

7.SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\*
1. \$IDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1989.DAT:\*
2. \$IDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1991.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

A surface protein	N. meningitidis H3	A surface protein	N. meningitidis Hl	A surface protein	N. meningitidis BZ	A surface protein	N. meningitidis BZ	A surface protein	BASB029 amino acid	N. meningitidis EG
	AAU06176	AAY23742	AAU06177	AAY23738	AAU06178	AAY23739	AAU06179	AAY23740	AAY57044	AAU06174
20	22	20	22	20	22	20	22	20	21	22
599	599	598	598	598	598	594	594	594	594	594
100.0	100.0	92.3	92.3	92.2	92.2	91.6	91.6	90.3	90.3	90.3
3060	3060	2824.5	2824.5	2821.5	2821.5	2802.5	2802.5	2762.5	2762.5	2762.5
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	100.0 599 20 AAY23743	100.0 599 20 AAY23743 100.0 599 22 AAU06176	100.0 599 20 AAY23743 100.0 599 22 AAU06176 92.3 598 20 AAX23742	100.0 599 20 AAY23743 100.0 599 22 AAU06176 92.3 598 20 AAY23742 92.3 598 22 AAU06177	100.0 599 20 AAY23743 100.0 599 22 AAU06176 92.3 598 20 AAY23742 92.3 598 22 AAU06177 92.2 598 20 AAX23738	100.0 599 20 AAY23743 100.0 599 22 AAU06176 92.3 598 20 AAY23742 92.3 598 22 AAU06177 92.2 598 22 AAV23738	100.0 599 20 AAY23743 100.0 599 22 AAV06176 92.3 598 20 AAY23742 92.3 598 22 AAU06177 92.2 598 22 AAU06177 91.6 594 20 AAY23739	100.0 599 20 AAY23743 100.0 599 22 AAU06176 92.3 598 20 AAY23742 92.2 598 22 AAU06177 92.2 598 20 AAY23738 91.6 594 20 AAY23739 91.6 594 22 AAU06179	100.0 599 20 AAY23743 100.0 599 22 AAU06176 92.3 598 20 AAX23742 92.2 598 22 AAU06177 92.2 598 22 AAV06178 91.6 594 20 AAX23739 91.6 594 22 AAV06179 90.3 594 20 AAX23740	AAY23743 AAU06176 AAX23742 AAX23738 AAU06178 AAX23739 AAX23739 AAX23739 AAX27740 AAX57740

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112 114 115 116 118	50 50 50 50 50 50 50 50 50 50 50 50 50 5	333 333 33 33 33 33 33 33 33 33 33 33 3	V 8 0 0 H 1 M 4 M

## ALIGNMENTS

Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide. A surface protein of Neisseria meningitidis. AAY23743 standard; Protein; 599 AA. Peak IRA; (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND. 98WO-AU01031. 97GB-0026398. (first entry) Jennings MP, Moxon ER, Neisseria meningitidis. WPI; 1999-418754/35. N-PSDB; AAX85795. WO9931132-A1 14-DEC-1998; 12-DEC-1997; 08-SEP-1999 24-JUN-1999. AAY23743; AAY 23743 RESULT 

Neisseria meningitidis surface proteins useful for treating N. meningitidis infections

"Conserved region 1"

/label= Cl

Location/Qualifiers

Key Region

"Conserved region 2"

/label= C2

.117

Region

5

"Variable region

'label= v2

'note=

.131

Region

'note=

132..195 /label= C3

Region

-

region

/label= V1 /note= "Variable

51..105

Region

'note=

"Conserved region 4"

243

Region

 $^{\circ}$ 218..236 /label= C

"Conserved region 3"

217

Region

'note⇒

/label= V3 /note= "Variable region 3"

'note-/note=

Region

/label= C5 /note= "Conserved region 5"

25-JAN-2001; 2001WO-AU00069 25-JAN-2000; 2000US-0177917

WO200155182-A1. 02-AUG-2001. (UYQU ) UNIV QUEENSLAND.

Jennings MP;

Peak IRA,

2001-488774/53.

N-PSDB; AAS09166

4 "

/label= V4 /note= "Variable region

244..599

Region

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Claim 1; Page 114-115; 132pp; English
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigon Nhh and AAU06182-AAU06186). The modified or mutant Nhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophlactic vacchnes against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains then would be expected from a corresponding wild-type surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 7.9e-171;
ive 0; Mismatches 0;
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New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -

Claim 9; Fig 1; 91pp; English.

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Surface antigen NhhA; meningococcal disease; meningitis vaccine

Neisseria meningitidis strain H38

N. meningitidis H38 surface antigen NhhA polypeptide sequence.

(first entry)

24-OCT-2001 AAU06176;

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AAU06176 standard; Protein;

AAU06176

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       GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
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N-PSDB; AAX85794.
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                                The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               481 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                                                                                                                                                                                                                                                                                                                1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     480 kdankpvritnvapgvkegdvtnvaqlkgvaqnlnnridnvdgnaragiaqaiataglaq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                              Score 2824.5; DB :
Pred. No. 4.4e-157,
14; Mismatches 29,
Page 108-110; 132pp; English
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Best Local Similarity
Matches 555; Conserv
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Gaps

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29; Indels

14; Mismatches

Matches 555; Conservative

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhA (AAU06186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhA from N. meningitidis strain H15 is 1 of 10 NhA polypeptide sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                        i...Co.
/label= Cl
/arte= "Conserved region 1"
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195..216
/label= V3
^^= "Variable region 3'
           Neisseria meningitidis strain H15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JAN-2000; 2000US-0177917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention.
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N-PSDB; AAS09167.
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                                   Key
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17..235 |label= C4 note= "Conserved region 4"

label= C3 note= "Conserved region 3"

5

label= V2
note= "Variable region

31..194

17..130

/label= C2
/note= "Conserved region 2"

05..116

il..104 /label= V1 /note= "Variable region

.ocation/Qualifiers

/label= V4
/note= "Variable region

36..242

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240
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                                                                   241 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG 300
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                                                                                                                                                  KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG 360
                                                                                                                                                          EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120
                                                                                                                                                                               361 KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 420
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DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
                                                          KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
                                                                                                                             glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                      A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peak IRA;
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QUEENSLAND.
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                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                             immunoreactive peptide
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N-PSDB; AAX85790.
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(UYQU ) UNIV
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Length 598;

Score 2824.5; DB 22; Pred. No. 4.4e-157;

92.3%; 92.7%;

Query Match Best Local Similarity

Mon Jul

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meningitidis surface proteins useful for treating

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EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120
                                                                                                                                                                                                                                                                                                                                                                                                         ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG 300
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                         meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
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                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                          20; Length 598;
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                                                                         protein of Neiserria
                                                                                                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                       ; Score 2821.5; DB ;
; Pred. No. 6.5e-157;
13; Mismatches 30;
                                                                           sequence represents a surface
                                              Claim 1; Page 91-93; 132pp; English.
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                                                                                                                                                                                                                                                                Matches 555; Conservative
                      meningitidis infections
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239

420

419

359

540

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhA (AAV06186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain BZ10 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
            meningococcal disease; meningitis vaccine.
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/label= Cl
'note= "Conserved region l"
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/note= "Conserved region 2"
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/note= "Conserved region 4"
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| Note= "Conserved region
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/note= "Variable region
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                                                             .ocation/Qualifiers
                                    Neisseria meningitidis strain BZ10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JAN-2000; 2000US-0177917.
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217..23
            Surface antigen NhhA;
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Sequence

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(first entry)
 WPI; 1999-418754/35.
N-PSDB; AAX85791.
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                                                                                                                                                    Similarity
                                                                                                                         594 AA;
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Matches 554;
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                                                                                                                          Sequence
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                                                                                                                                                                                                                                                  KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ 540
                                                       EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120
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                                                                                                                                                                                                                                                                           GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS
                                                                                                                                                                                                                                                        KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
                                                                                                                                       ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG
                                                                                                                                                                  KGENGSSTDEGEGLVTAKEV IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
                           1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                   DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
  Length
                                                                                                                                                                                                                                                                                                                                                                                 surface glycoprotein; infection; vaccine;
               Indels
  22;
Score 2821.5; DB 2
Pred. No. 6.5e-157;
                                                                                                                                                                                                                                                                                                                                                                    A surface protein of Neisseria meningitidis.
              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peak IRA;
              13;
                                                                                                                                                                                                                                                                                                                           AAY23739 standard; Protein; 594
92.28;
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INNOVATION QUEENSLAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moxon ER,
                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                        immunoreactive peptide
       Similarity
                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIND ( DŌAD)
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                                                                                                                                                                                                                                                                                                                                                                                                                               24 - JUN-1999
              555;
 Query Match
Best Local
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             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       481 KDANKPVRITHVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
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                                                                                                                                                                                                                                                                                                                                                                       DB 20; Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                               5,
ż
treating
surface proteins useful for
                                                                                                                                                                                                                                                                                                                                                   91.6%; Score 2802.5; DB 20
92.5%; Pred. No. 8.3e-156;
wiematches 28;
                                                           English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
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                                                           Claim 1; Page 95-97; 132pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                   meningitidis infections
Neisseria meningitidis
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2;

5

Gaps

5

175

/label= C2

..116

/label= v2

.126

note=

240 235 295

180

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Claim 9; Fig 1; 91pp; English.
                                                                                                                        25-JAN-2001; 2001WO-AU00069
                                                                                                                              25-JAN-2000; 2000US-0177917
                                                                                                                                    (UYQU ) UNIV QUEENSLAND
                                                                                                                                          Peak IRA, Jennings MP;
                                                                                                                                                                                                                    he present invention.
                                                                                                                                                WPI; 2001-488774/53.
N-PSDB; AAS09169.
                                                                                                            WO200155182-A1
                                                                                                                  02-AUG-2001
                       Region
                                 Region
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594 AA;

Sequence

594

..231

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KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 420
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                                                                                  541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDANKPVRITUVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                                                                                                                                                                 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; surface glycoprotein; infection; vaccine;
                                                   Indels
                  DB 22;
              91.6%; Score 2802.5; DB 22
larity 92.5%; Pred. No. 8.3e-156;
Conservative 12; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A surface protein of Neisseria meningitidis.
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                               Best Local Similarity
Matches 554; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9931132-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY23740;
                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain B1198 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel Neisseria
                                 Surface antigen NhhA; meningococcal disease; meningitis vaccine.
N. meningitidis BZ198 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                       /notc
|127.190
|/label= C3
|^^^+e= "Conserved region 3"
                                                                                                                                      /label= Cl
/note= "Conserved region 1"
                                                                                                                                                                                                                                                                "Conserved region 2"
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                                                                                                                                                                       51..104
/label- Vl
/note- "Variable region
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/label= V4
/note= "Variable region
                                                                                                                                                                                                                                                                                                                                                                                                        /label= V3
/note= "Variable region
                                                                    Neisseria meningitidis strain BZ198
                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= C4
/note= "Conserved
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540

BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.

/note= "Encoded by AATC"

Location/Qualifiers 104

Misc-difference

WO9958683-A2

Neisseria meningitidis.

BASB029; Nisseria

BASB029 amino acid sequence from N. meningitidis strain ATCC13090.

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21-FEB-2000

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                                                                                                                                                                                                                                                                                                                                                               - ntnentnassftyslkkdltdltsvgteklsfsansnkvnitsdtkglnfakktaetng 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kgttatvskddggnitvmydvnvgdalnvnglqnsgwnldskavagssgkvisgnvspsk 415
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                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                      1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60
                                                                                                                                                                                                                                                                                541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                    KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 594;
                                                                                                                                                                                                                                                    .;
2
                                                                                                represents a surface protein of Neiserria
                                                  ż
                                                surface proteins useful for treating
                                                                                                                                                                                                                               Score 2762.5; DB 20; Lengt
Pred. No. 1.8e-153;
3; Mismatches 32; Indels
                                                                             Claim 1; Page 100-101; 132pp; English.
 Peak IRA
                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                               90.3%;
91.7%;
                                                                                                                                                                                                                                                    Conservative
Moxon ER,
                                                Neisseria meningitidis
meningitidis infections
                                                                                                 present sequence
                   WPI; 1999-418754/35.
                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                 594 AA;
                             N-PSDB; AAX85792
 Jennings MP,
                                                                                                                                                                                                                                          Best Local Sim
Matches 549;
                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                Query Match
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New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal

Claim 4; Fig 2; 74pp; English.

(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

WPI; 2000-053103/04.

Ruelle J;

N-PSDB; AAZ39864

99WO-EP03255. 98GB-0010276

07-MAY-1999;

13-MAY-1998;

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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the serogroup B strain ATCC13090. The BASB029 protein is homologous to the amembhilus influences surface fibril (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAX57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune collingitidis infection in a mammal. Composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an confinence of infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 colynucleotide, and for therapeutic or prophylactic purposes, particularly bacterial infections. The protein is useful in the combinant correction is useful for treating and development of antibacterial drugs. Fused recombinant correction is useful for the stimulation of the immune system of an organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2762.5; DB 21
Pred. No. 1.8e-153;
3; Mismatches 32;
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91.7%;
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Best Local Si
Matches 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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AAY57044 standard; Protein; 594

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AAY57044

AAY57044;

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25-JAN-2001; 2001WO-AU00069 25-JAN-2000; 2000US-0177917

WO200155182-A1. 02-AUG-2001 (UYQU ) UNIV QUEENSLAND

Peak IRA,

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480
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                                                                                                                                        KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ 540
                                ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG 300
                                                                                                                                                                                                541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 599
                                                                                                                                                                                                         DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
                                                                                                                                 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS
                                                                                                 KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                                                                                                                                                                        Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                         N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                 'note= "Conserved region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Conserved region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                          "Variable region 1"
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/note= "Conserved region
                                                                                                                                                                                                                                                                                                                                                                                                                                        117 . 126
/label= V2
/note= "Variable region
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/note= "Variable region
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                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis strain EG327
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                                                                                                                                                                                                                                                         AAU06174 standard; Protein; 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127..190
/label= C3
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/label= C4
                                                                                                                                                                                                                                                                                                                                                                                         51..104
/label= V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= C5
                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                         /label= Cl
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AANO6186. The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the whild type surface antigen NhhA from N. meningitidis strain S0317 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235
                                                                                                                                                                                                                                              New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 594;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.3%; Score 2762.5; DB 2 91.7%; Pred. No. 1.8e-153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                                                                                                                                                                                Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    549; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the present invention.
                                                                                                                                                                                               WPI; 2001-488774/53
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Best Local Similarity
Matches 549; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 AA;
                                                                                                                                                                                                               N-PSDB; AAS09164.
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KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK 

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421

KGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTTANGQTGQADKFETVTSGTNVTFASG

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GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS 480

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                                                                                                                                                   300 GKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFAS
                                                                                                                                                                 420 KGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVG
                                                                                                                                                                                                                                                                                                                  480 SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
                                                                                                                                                                                                                                                                                                                                                                       540 QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                         GDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGT
                                                                                                          disease; meningitis vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein, specifically 12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  meningitidis H41 surface antigen NhhA polypeptide sequence.
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/note= "Variable region 3"
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/note= "Conserved region
115..124
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/nnte= "Conserved region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Predicted mature claimed in claim 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..51
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Surface antigen NhhA; meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52..592
/label= Mature_NhhA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis strain H41.
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/note= "Conserved
189..210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211..229
/label= C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= V2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
AAU06172 standard;
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               115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 NKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTN 179
  416 gkmdetvninagnnieitrngknidiatsmtpqfssvslgagadaptlsvddegalnvgs 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                  599
                                                                                               a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; Length 592;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                          Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 88.2%; Score 2699.5; DB 20 Best Local Similarity 91.2%; Pred. No. 8.5e-150; Matches 547; Conservative 11; Mismatches 33;
                                                                                                                                                                                                                                                               surface protein of Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 118-120; 132pp; English.
                                                                                                                                                                                 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peak IRA;
                                                                                                                                                                                592
                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INNOVATION LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ISIS-) ISIS INNOVATION (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moxon ER,
                                                                                                                                                                                                                                                                                                       immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-418754/35
                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      592 AA;
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                                                                                                                                                                                                         AAY23744;
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532

599 592

479 472 539

Page 11

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gkgengsstdegeglvtakevidavnkagwrmktttangqtgqadkfetvtsgtkvtfas 352
                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
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                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AdMUGOISEA-ANUGOISE). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain H 11 is 1 of 10 NhhA polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHG-ATVTLKAGDNLKIKQNT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTN 179
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                                                                                                                                                                                                                                                          or
                                                                                                                                                                                                                                             New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.2%; Score 2699.5; DB 2
91.2%; Pred. No. 8.5e-150;
ive 11; Mismatches 33;
 "Conserved region 4"
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/note= "Conserved region
230..236
/label= V4
/note= "Variable region
                                     737..592
/label= C5
/note= "Conserved
                                                                                                                                                                                                                                                                                       Claim 9; Fig 1; 91pp; English.
                                                                                                                            25-JAN-2001; 2001WO-AU00069
                                                                                                                                                 25-JAN-2000; 2000US-0177917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 547; Conservative
                                                                                                                                                                      (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                           Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     he present invention.
                                                                                                                                                                                                             WPI; 2001-488774/53.
N-PSDB; AAS09162.
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                                                                                  WO200155182-A1
                                                                                                       02-AUG-2001.
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           Region
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BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
                                                                                                                                     472
                                                                                                                                                                                                                                                                           599
                                                                                                                                                                                                                                                                                                     This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention
540 QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                          KGKMDETVNINAGNNIEITRNGKNIDIATSMTPOFSSVSLGAGADAPTLSVDDKGALNVG
                                                                                                                                                                                     SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASB029 amino acid sequence from N. meningitidis strain H44/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by AATC'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Encoded by AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by GAT"
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Surface protein; surface glycoprotein; infection; vaccine;

Veisseria meningitidis. immunoreactive peptide.

W09931132-A1

24-JUN-1999

Peak IRA;

Moxon ER,

Jennings MP,

WPI; 1999-418754/35

N-PSDB; AAX85797

INNOVATION LID. 97GB-0026398

(ISIS-) ISIS INNOVATION (UYQU ) UNIV QUEENSLAND

98WO-AU01031.

14-DEC-1998; 12-DEC-1997;

surface protein of Neisseria meningitidis.

(first entry)

08-SEP-1999

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relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism.
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89.9%; Pred. No. 1.4e-149;
iive 14; Mismatches 33;
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Best Local Simi.
Matches 541; (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 589;
                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis surface proteins useful for treating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.0%; Score 2694; DB 20;
89.7%; Pred. No. 1.8e-149;
iive 14; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 122-124; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 89.7
Matches 539; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    meningitidis infections
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AAY23745 standard; Protein; 589

RESULT 15

AAY23745 ID AAY2

3;

Search completed: July 3, 2002, 08:09:11 Job time: 497 sec ATE SE'

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GenCore version 4.5
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OM protein - protein search, using sw model

July 3, 2002, 08:10:19; Search time 64.11 Seconds (without alignments) 228.216 Million cell updates/sec Run on:

US-09-771-382-6 3060 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 599 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

231628 seqs, 24425594 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 15, Appl	Sequence 15, Appl	13,	13,	5,	'n	7	7,	Sequence 9, Appli	6	17,	17,	19,	19,	21,	21,	11,	Sequence 11, Appl	2, A	7	Sequence 33, Appl	4	33,	47,	36,	6, 2	Sequence 6, Appli
SUMMARIES	QI ;	US-09-377-155-15	US-09-669-974-15	US-09-377-155-13	US-09-669-974-13	US-09-377-155-5	US-09-669-974-5	US-09-377-155-7	US-09-669-974-7	US-09-377-155-9	US-09-669-974-9	US-09-377-155-17	US-09-669-974-17	US-09-377-155-19	US-09-669-974-19	US-09-377-155-21	US-09-669-974-21	US-09-377-155-11	US-09-669-974-11	US-09-377-155-2	US-09-669-974-2	US-09-377-155-33	US-08-913-942-4	US-09-669-974-33	US-09-268-347-47	US-09-268-347-36	US-08-409-995-6	US-08-685-467-6
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	Score	3060	3060	2824.5	2824.5	2821.5	2821.5	2802.5	2802.5	2762.5	2762.5	2699.5	2699.5	2694	2694	2685	2685	2676	2676	2663.5	2663.5	1271	1271	1271	1270	1246	1199.5	1199.5
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                                     KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
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ilarity 100.0%; Pred. No. 7.2e-233;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                 APPLICANT: PEAK, IAN Richard Anselm, APPLICANT: DENNINGS, Michael Paul, APPLICANT: DENNINGS, Michael Paul, APPLICANT: DENNINGS, Michael Paul, APPLICANT MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SED ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                   Sequence 15, Application US/09669974 Patent No. 6333173
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                  240 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKG
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KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALENTIN VET. 2.0
SOFTWARE: PALENTIN VET. 2.0
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                                 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR PLING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
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SEMENTAL INFORMATION:
APPLICANT: DENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, EN RICHARD
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1999-12-13
SOFTWARE: PATENTIN NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN Ver: 2.0
                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
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Matches 555; Conservative
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US-09-669-974-13
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                             US-09-377-155-7; Sequence 7, Application US/09377155; Patent No. 6197312; GENERAL INPORMATION:
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Matches 554; Conservative
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
ITILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 66564/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
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PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.0
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Patent No. 6333173
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US-09-669-974-5
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Best Local Similarity 92.7%
Matches 555; Conservative
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LENGTH: 598
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APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MONON, E. Richard
TILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCHIN VET. 2.0
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                                                                                                                                                             Sequence 9, Application US/09377155 Patent No. 6197312
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Best Local Similarity 91.7%.
Matches 549; Conservative
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CURRENT APPLICATION NUMBER: US 09/377,155

PRIOR PILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

SOFTWARE: PATENTING UND NUMBER: GB 9726398.2

SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                            Sequence 7, Application US/09669974
Patent No. 6333173
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Matches 554; Conservative
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Pred. No. 1.9e-209;
3; Mismatches 32;
                                                                                                        APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXOM, E. Richard
TILLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
                                                                      Sequence 9, Application US/09669974 Patent No. 6333173
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US-09-669-974-9
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ilarity 91.7%;
Conservative 1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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                                                                                                  GENERAL INFORMATION:
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11; Mismatches 33
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                                                                                                                                      GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXOM, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
                                                                                                 Sequence 17, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Neisseria meningitidis US-09-377-155-17
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SOFTWARE: Patentin Ve
SEQ ID NO 17
                                                         RESULT 11
US-09-377-155-17
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%; Pred. No. 1.7e-204;
11; Mismatches 33;
                                             GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR PELING DATE: 1999-08-19
PRIOR PELING DATE: 1998-12-14
PRIOR PELING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SCFTWARE: PATENTIN Ver: 2.0
SEQ ID NO 17
LENGTH: SA
            Sequence 17, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Neisseria meningitidis US-09-669-974-17
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.2%;
Best Local Similarity 91.2%;
Matches 547; Conservative 11
                                           GENERAL INFORMATION:
US-09-669-974-17
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241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTG 298
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Pred. No. 4.6e-204;
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                                                         APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MONON, E. Richard
TITLE OF INVENTION: NOVEL SUBFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
; Sequence 19, Application US/09377155
; Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Neisseria meningitidis US-09-377-155-19
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SOFTWARE: Patentin Ve
                                             GENERAL INFORMATION:
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LENGTH: 589
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; Pred. No. 4.6e-204;
14; Mismatches 34;
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); CURRENT PEDLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR PILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR PILING DATE: 1998-12-14
; PRIOR PILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
                                                                    APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
                            Sequence 19, Application US/09669974
Patent No. 6333173
                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Neisseria meningitidis US-09-669-974-19
                                                                                                                                                                                                                                                                                                                                                                                    88.0%;
89.7%;
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Best Local Similarity 89.7%
Matches 539; Conservative
                                                         GENERAL INFORMATION:
RESULT 14
US-09-669-974-19
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PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALN 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 NINKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASGRGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.7%; Score 2685; DB 4; Length 591;
89.4%; Pred. No. 2.4e-203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                        APPLICANT: PEAK, Tan Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: DENNINGS, Michael Paul APPLICANT: MONON, E. RICHARD TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
FILE REFERENCE: 065064/0128
FUNERNY FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-112-12
PRIOR FILING DATE: 1997-112-12
PRIOR FILING DATE: 1997-112-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Pred. No. 2.4e
16; Mismatches
Sequence 21, Application US/09377155
Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 89.4
Matches 538; Conservative
                                                                                                                                                                                                                                                                                                                            Patentin Ver.
                                        ; GENERAL INFORMATION:
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14;

237

177

290

357

297

417

469 537 529

11 Db 590 QW 591

Search completed: July 3, 2002, 08:10:21 Job time: 533 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 3, 2002, 08:12:25; Search time 95.27 Seconds (without alignments) 604.151 Million cell updates/sec Run on:

US-09-771-382-6 3060 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 599

Title: Perfect score: Sequence: Scoring table:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

				•																									
Description	adhesin NMB0992 (i	probable surface f	adhesin homolog HI	surface protein XF	probable autotrans	surface protein XF	probable adhesin 2	probable adhesin E	probable surface p	o pasodx	190K surface antiq	hypothetical prote		AidA-I adhesin-lik	probable adhesin Z	ydeK protein - Esc	adhesin AIDA-I pre	probable adhesin h	190-KDa cell surfa	hypothetical prote	probable autotrans	hypothetical prote	outer membrane pro	probable invasin Y	surface-array prot	high-molecular-wei	high-molecular-wei	hypothetical prote	
OUTGARLES	G81133	A81888	I64138	A82615	AC0976	D82671	A86036	н91188	АН0110	C82672	A41477	G64964	T31105	D90803	н85611	A64905	S28634	AF0394	A97859	B98047	AD0123	AG2560	T30852	AB0480	A56143	A43855	B43855	D85724	E90893
DB	7		7											•						7									
Length	591	592	298	1190	1107	2059	1588	1588	658	1004	2249	1091	4919	949	1005	1325	1286	1910	2021	2551	3705	1487	1029	3013	1109	1536	1477	1343	1343
% Query Match	87.7	84.6	19.7	13.4	13.3	13.3	12.1	12.1		•	7.9	7.8	7.5	7.5	7.5	7.5	7.4	7.2	7.2	7.1	7.0	7.0	7.0	7.0	6.9	6.9	6.7	6.7	6.7
Score	2685	2587.5	601.5	410.5	404	406.5	369.5	369.5	341	264.5	241	240	231	228	228	228	225.5	221.5	221.5	217.5	215	213.5	213	213	211	210	206	204.5	203.5
Result No.		7	М	4	S	9	7	8	δ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	sapB protein - Cam	hypothetical prote	surface-array prot	hemolysin (importe	crystalline surfac	hypothetical prote	hypothetical prote	puative autotransp	ABC-type transport	IgA-specific metal	hemagglutinin/hemo	flagellin (importe	hypothetical prote	probable RTX famil	cell surface prote
F90696	I40711	AH2515	A37284	AI0452	JN0896	E97835	876109	AD0548	C48399	S57664	F81045	F90961	F85809	B85547	AB3486
7	~	7	7	7	7	~	7	7	7	~	~	7	7	7	7
5291	936	4936	893	1635	1645	1655	3029	961	2020	1366	2514	585	585	5188	365
9.9	9.9	9.9	9.9	9.9	6.5	6.5	6.5	6.5	6.5	6.4	6.4	9	6.4	6.4	6.3
203	202.5	202.5	201.5	201.5	200	199.5	199.5	199	197.5	197	197	196.5	195.5	194.5	193.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

	RESULT 1 G81133 adhasin NMB0992 C;Species: Neis C;Date: 31-Mar- C;Accession: G8 R;Tettelin, H.; H;Cept. H.; Qin, H. ri, H.; Qin, H. science 287, 18 Authors: Gran A;Title: Comple A;Reference num A;Reference num A;Reference num A;Residues: 1-5 A;Cross-referen A;Experimental C;Genetics: A;Genetics:	RESULT 1  GB1133  adhesin NMB0922 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  CiSpecies: Neisseria meningitidis  CiSpecies: Neisseria meningitidis  CiDate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001  CiDate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001  CiDate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001  CiAccession: GB1133  CiAccession: GB1133  Aithory Ex.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.  Cidence 287, 1869-1815, 2000  Aithors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  A; Reference number: AB1000; MUID:20175755  A; Rocession: GB1133  A; Molecule type: DNA  A; Regeriamental source: serogroup B, strain MC58  C; Genetics:  A; Experimental source: serogroup B, strain MC58  C; Genetics:  CiSpecial Aight
	Query Match Best Local Matches 53	Query Match Best Local Similarity 89.4%; Pred. No. 1.9e-129; Matches 538; Conservative 16; Mismatches 34; Indels 14; Gaps 4;
	Qy 1 Db 1	1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEF- 59 
-	Qy 60 Db 61	60 -LEPVVRSALVLOFMIDKEGNGENEST-GNIGWSIYYDNHNTLHGATVTLKAGDNLKIKO 117  :    :
	Oy 118 Db 121	118 NTNKNTNENTNDSSETYSLKKDLTDLTSVETEKLSFGANGNKVNITSDFKGLNFAKETAG 177   ::
	Oy 178 Db 171	3 TNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKP 237 
	Qy 238 Db 231	3 GTTASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT 297 
	Qy 298 Db 291	298 GKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRWKTTTANGQTGQADKFETVTSGTNVTF 357 11 41111111111111111111111111111111111

358 ASGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 417

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probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09.Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C; Accession: Ac0976 R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A; Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Reference number: AB0502; PMID:11677608 A; Reference number: AB0502; PMID:11677608 A; Accession: Acoession: Acoession: Accession: Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-1107 <PAR>
A; Resicus references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
C; Genetics:
A; Gene: sapB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 ESTGNIGWSIYYDNHNTLHGATVTLK ----AGD------NLKIKQNTN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 LSSDNLSWNETTNSFSASHGSSTTNKITNVAAGELSEESTDAVNGSQLFETNEKVDQNTT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ---KNTNENTNDSSFTYSLKKDLTDL-TSV------ETEKLSFGAN--GNKVNITS 164
273 TFSASRNGSASKITNLAAGTLAADSTDAVNGSQLYETNQKVDQNTSAI---ADINTSITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIKGLNFAKETAGING----DITVHLNGIGSTLIDILLNTGATINVINDNVIDDKKKRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSTSNRAITTGIRETSATSDGVVIGYNTTDRELLGALSLGTDGESYRQITNVADG--SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKDVLNAGWNIKGVKPGTTASDNVDFVH---TYDT-----VEFLSADTKTTTVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTGVKYIRTNDNGLEGQDAYATGNGATAVGYDAVASGAGCLALGONSSSSIEGSIALG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 TKRASATVKTAVLATLLFATVQANATDEDEEEEL----EPVVRSALVLQFMIDKEGNGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384 GDALNVNQLQN--SGWNLDSKAVAGSSGKVISGNVSP-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.3%; Score 407; DB 2; Lk Best Local Similarity 22.1%; Pred. No. 3.3e-13; Matches 188; Conservative 116; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 ADKFETVTSGTNVTFASGKGTTATVSKDDQGNIT---
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                                                                                                                                                                                      A; Status: preliminary
A; Nobecule type: DNA
A; Residues: 1-190 (SIM>
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Rehnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; A; Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Tsuhako, M.H.; Vallada, H.; Van Silva, F.R.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .015 PIAAGVDATAIGVGATASGADSIAMGNKASASADNAVAIGNHSVADRANTVSVGSAGSER 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   393 ----QNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIAT 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          927 ARGAESYTGKYSGLQNNTVGTVSVGDASKGETRTVS-----NVADAKEAT--DAVNLRQL 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              449 SMTPQFSSVSLGAGADA------PTLSVDDKGAL------NVGSKDANK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   706 AVNFSQLQAVSSTASKGWNLLASGANSSNVAPGESVDLKNTDGNIVISKESGSNDVLFNL 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274 GKRTEVKIGAKTSVIKEKDGKLVTGKGKGENG-SSTDEGEGLVTAKEVIDAVNKAGWRMK 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 STGNIGWSIY---YDNHNTLHGATVTLKAGD-NLKIKQNTNKNTNENTNDSSFTY--SLK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GNK--VNI---TSDTK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G-WNIKGVKPGTTASDNVDF------VHTYDTVEFLSADTKTTVNVESKDN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSQKITNVAAGTADTDAVNLSQLNTAMAGSGAKSVHYYSTYD---GGTQGGNYNGDGATG 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                        A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: A82615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542 YLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 599
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; Pred. No. 2.4e-13;
88; Mismatches 206;
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24.8%;
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Best Local Similarity 24.89
Matches 163; Conservative
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0 QY 275 KRTEVKIGAKTSVIKEKDCKLVTCKGKGENGSSTDEGEGLVTAKEVIDAVNKA 8	Oy 328 GWRMKTTANGOTGOADKFETVISGINVTFASGKGTT	Oy 365 -ATVSKD	OY 385DALMVNQLQNSGWNLDS	Qy         425 ETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGAL 476           ::         ::         ::           ::	Qy 477 NVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQA 532 11	ucleotide Sequen  Qy 533 IATAGLVQAYLPGKSMMAIGGGTYRGEAGYALGYSSISDGGNWIIKGTASGNSRGHFGAS 592	Qy 593 ASVGYQW 599                   Db 2053 AGVGYQW 2059	3:GN001	C; Accession: A86036  C; Muyaki, C; X;  A; Reference number: A85480; MUID: 21074935; PMID: 11206551  C; Accession: A86036  C; Accession: A86036  C; Accession: A86036  C; Accession: A86036  C; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Rose, D	Silveir A.L.; Z	32;
Db 861 IENGIGDIVTTGSTKYFKTNTDGADANAQGADSVAIGSGSIAAAENSVALGTNSVADEAN 92 QY 475 ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLK	Qy 509GUAQ	QY 531 QAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGWUIKGTASGNSRGHFG 59 1:1	591 ASASVGYQW 599	DD 1099 AAIGAGFUW 110/ RESULT 6	DB2671 Surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa C;Species: Aylella fastidiosa C;Species: Aylella fastidiosa C;Species: Aylella fastidiosa	Rancommons, The Xylella fastidiosa Consortium of the Organization for Nu Nature 406, 151-157, 2000 A.Title: The genome sequence of the plant pathogen Xylella fastidiosa.	#; Reterence number: A82312; MU10:2U302/1/ A; Note: for a complete list of authors see reference number A59328 below A; Accession: D82671 A; Status: preliminary A; Molecule type: DNA	A; Residues: 12059 (SIM)> A; Cross-references: GB:ARO3982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. R; Simpson, A.J.G.; Reinach, F.C.; Arruda, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; Bl-Dorry, H.; Facthcanl, A.P.; Ferreira, A.J.S.	submitted to GenBank, June 2000 A.Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C., J.D.; Junqueira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E., Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Mariakuthors, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, F.G.; Nunes, L.R.; Oliveira, M.A.Y.; Meo Oliveira, M.C.; de Oliveira, R.C.; Palmies, R.C.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; S.	A.Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; V A.Reference number: A59328 A.Contents: annotation C.Genetics: A.Gene: XF1529	Query Match         13.3%;         Score 406.5;         DB 2;         Length 2059;           Best Local Similarity         25.5%;         Pred. No. 7.8e-13;           Matches         170;         Conservative         93;         Mismatches         219;         Indels 185;         Gaps           Qy         89         GWSIYYDNHNTHGATYTLKAGD-NLKIKQNTNKNTNENTNDSSFTYSL 136

us-09-771-3\\ 2-6.std.rpr

1128	RESULT 9  ANOLIO  Probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain C092) C; Species: Yersinia pestis C; Species: Oz-Nov-2001 C; Species: Versinia pestis C; Species: Versinia pestis C; Species: Versinia pestis C; Species: Versinia pestis C; Date: Oz-Nov-2001 C; Accession: AH0110 C; Accession: AH010 C; Accession: AH01010 C; Accession: AH01010 C; Accession: AH01010 C; Accession
Db 1128 ENGVVIGYDTTDGELLGALSIGDDGKYRQIINVADGSEAHDAVTVROLQNAIG 1180  Qy 248 -VHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLV 296  1181 AVATTPTRYEHANSTEDSLAGT	HESULR 8 H91188 H91188 H91188 H91188 H91188 H91188 H91188 H91188 H91188 H91189 H91989 H91999 H9199

Db 120 FSKAFAPNAIALGYNSSVTQSANNGVALGSNSTVSGVNSVALGAGSMA 167  Qy 158 NKVNITSDTKGLNFAKETAGTNGDTTVHLNGIGSTLFDTLLNTGATTNVTNDNVTDDKKK 217  :::::::::::::::::::::::::::::::::::	QY         448 TSMTPQFSSYSLGAGADAPTLSVDDKGALNVGSKD-ANKPV-RITNVAPGVKEGDVTNV 504           I         I:	RESULT 11  A41477  190K surface antigen precursor - Rickettsia rickettsii  C;Species: Rickettsia rickettsii  C;Species: Rickettsii  C;Species: Rickettsii  C;Species: Rickettsii  C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 08-Oct-1999  C;Accession: A41477  R;Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.  Infect. Immun. 58, 2760-2769, 1990  A;Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated, A;Reference number: A41477; MuID:90354033  A;Recession: A41477  A;Molecule type: DNA  A;Residues: 1-249 cANDA  C;Reywords: surface antigen; tandem repeat  C;Keywords: surface antigen; tandem repeat  F;1-20/Domain: signal sequence (uncleaved) #status predicted <sigu></sigu>	Query Match  Query Match  Best Local Similarity 23.9%; Score 241; DB 2; Length 2249;  Best Local Similarity 23.9%; Pred. No. 0.00023;  Matches 165; Conservative 72; Mismatches 275; Indels 178; Gaps 34;  QY 10 NSALNAWVAVSELTRNHTKRASATVKT-AVLATLLFATVQANATDEDEEEELE 61
QY         301 KGENGSSTDEGECLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTNVTFASG 360           Db         384 SGDNGRCVENYIG           1:	es: Xylella fastidiosa 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 18-10-10-10-10-10-10-10-10-10-10-10-10-10-	M.C.; Frohm B.E.; Laigr Martins, E Miyaki, C.Y.; Pelmieri, D.P R.V.; Sawasak R.V.; Ga Silveir Core, A.L.; Z	Matches 159; Conservative 103; Mismatches 279; Indels 189; Gaps 33;  Qy 2 NRIYRIIMNSALNAWAVSELFRNHFRRASATVKTAVLATLLFATVQANATDED 55

	RESULT 13 T31105 hypothetical protein 2 - Haemophilus ducreyi C;Species: Haemophilus ducreyi C;Species: Haemophilus ducreyi C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999 C;Accession: T31105 R;Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J. J; Bacteriol. 180, 6013-6022, 1998 A;Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein. A;Reference number: 220984; MUID:99030326 A;Accession: T31105 A;Accession: T31105 A;Accession: T31105 A;Accession: Hanspire in A;Accession: C;Catus: Preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DA A;Residues: 1-4919 <aar> A;Cross-references: EMBL:AF057696; NID:93929021; PID:93929023; PIDN:AAC79761.1 C;Genetics: A;Gene: 1SpA2</aar>	Query Match         7.5%; Score 231; DB 2; Length 4919;           Best Local Similarity 22.4%; Pred. No. 0.002;           Matches 173; Conservative 91; Mismatches 268; Indels 240; Gaps 37;           QY 1 MNKIYRIHWNSALNAWV-AVSELTRNHTKRASATVKTAVLAT 41           i   I
76 111 111 111 111 111 111 111 111 111 1	RESULT 12  G64964  hypothetical protein b2000 - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 12-5ep-1997 #sequence_revision 17-5ep-1997 #text_change 02-Feb-2001 C;Accession: G64964  R;Blattner, F. R; Plunkert III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617 A;Reference number: A64720; MUID:97426617 A;Reference number: A64804 A;Status: nucleic acid sequence not shown; translation not shown A;Moleccule type: DNA A;Moleccule type: DNA A;Residues: 1-1091 <-BLAT> A;Cross-references: GB.AE000291; GB.U00096; NID:91788298; PIDN:AAC75061.1; PID:91788309; A;Experimental source: strain K-12, substrain MG1655 C;Keywords: nucleotide binding; P-loop F;683-690/Region: nucleotide-binding motif A (P-loop)	Ouery Match Best Local Similarity 21.9%; Score 240; DB 2; Length 1091; Best Local Similarity 21.9%; Pred. No. 0.0001; Matches 148; Conservative 80; Mismatches 249; Indels 200; Gaps 33;  Qy 1 MNIYRIUMNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60 1

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116 KONTN------KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGA---NGNKVNI 162
                                                                                                                                                     EENTGGQWIQNGGIAGNTTVTTNGRQVV-----LEGGTASDTVIRDGGGQSLNGLAVNT 149
                                                                                                                                                                                     163 TSDTKGLNFAKETAGTNGDTTVHLNGI-----GSTLTDTLLNTGATTNVTNDNVTDDKKK 217
                                                                                                                                                                                                                                                                                                                                                441 RGTLTLAAGGSLSGRTQLSKGASMVLNGDVVSTGDIVNAGEIRFDNGTTPNAALSRAVAK 500
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                                                                    325 GTNRLGNFTVENGKADGVVLESGGRLDVLESHSAQNTLVDDGGTLAVSAGGKATSVTITS
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                                                   EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNH----NTLHGATVT--LKAGDNLKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             GQTGQADKFETVTSGTNVTFASGK-------GTTATVSKDDQ-GNITVKY
RAASVKDVLN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000007; PIDN:BAB34819.1; PID:g13360856; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: ECS1396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         993 ADNITN-----DSNISNKIA-VLHSLGNISLNSKDQVYNLGEIYAGNNISVKAHQLKNDV 1046
                                                                                                                                                                                                   596 DNVTLNSKSTLSAGELTFKKVKNVTLNNDSELAANNLSLNASHNVTLNNKSKLSAQKADI 655
                                                                                                                                                                                                                                                                                                                                                                        336 ANGQIGQADKFE---TVTSGINVTFA-SGKGTTA-TVSKDDQGNITVKYDVNVGDALNV- 389
                                                                                                                                                                                                                                                                                                                                                                                               SKTKITNDGKLISIKNLNISSEADFINNGTLLGIEALKIATKGNFTNKEKAILASNSLLD 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSPSKGKMDETVN---INAGNNIEITRNGK--NIDIATSMTPQFSSVSLGAGADAPTLSV 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     882 ISVAEGK--KTFNNGTIESGKNLNITNTGAFLNVDNATIR-----SFGVLNITSTGNV 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNNGTLISNERLNITSAANFINESNGTVMSNGLLNIIAKQGNITNKNLIASRQQLNLTAV 992
 136 LENATVSANNLSFRVTNDTKLNNLSKVSARAADLQSGNLNLDKASVLAHKLTLNISNDVS 495
                                 94 YDNHNTLHGATVTLKAGDNLKIKQ-----NTNKNTNENTNDSSFTYSLKKDLTDLTSV 146
                                                                                                                                                                                                                                      ----VHTYDTVEFL--SADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTG--- 298
                                                                                                                                                                                                                                                                      KAVNLTLNDTTELTAKNLDINSTTTT----NNGTLAGIFANITTEKLNNKEKALILAEQN 711
                                                                                                                                                                                                                                                                                                                                       712 LNFTVNGSHYENKGDIVSKDKATVTFSKNSDFTSNGSKLVNAQN------QLKVNV 761
                                                                                                                              --NKSKFTAGNMTLNVTNNVT-LNNDSELAANNLTLNVTKNVTLNDASKLSANKLDLNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                           --NQLQNSG-----WNLDSKAVAGSSGKVI-----SGN-----SGN-
                                                        ---NVTDDKKKRAASVKDVLNAGWNIKGVKPGTTASDNVDF
                                                                                                                                                                                                                                                                                                         -----KGKGE-----NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDKGALNVGSK-DANKPVRITNVAPG------VKEGDVTN-----VAQLKGV
                                                                                                    ETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDTTVHLN---GIGSTLTDTLLNTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1047 KIMGDITTKTKEGQASYKLYQAS------NGGHFGNDGSSGY 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 546 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.5%; Score 228; DB 2; Length 949; Best Local Similarity 22.0%; Pred. No. 0.00034; Matches 180; Conservative 102; Mismatches 270; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQNLNNRIDNVDGNARAGIAQAIATAGLV - - - - QAYLPG - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-949 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
D90803
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485

297

----AG--WNIKGVKPGTTASDNVDFVH----TYD

384

----VNVGDALNVNQLQNSGWNLD----SKAVAG 406

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Cypecies: Escherichia coli
Cyspecies: Grocession: H85611; B85663
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Recession: H85611
A;Accession: H85611
A;Accession: H85611
A;Accession: H85611
A;Accession: H85611
A;Residues: 1-1005
A;Cross-references: GB:AE005174; NID:912514025; PIDN:AAG55356.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
PVRITNVAPG-----VKEGDVTNVAQLKGVAQNLNNRI------DNVDGNARAGIAQAI 533
                                                                                                                                                                                                                                                                                                                   534 ATAG-----LVQAYLPGKSMM----AIG------GGTYRGEAGYAIGYSS 568
                                                                                                                                                                               621 PLYTSMLTQAMDYDRILAGSRSHQTGVNGENNSVRLSIQGGHLGHDNNGGIARGATPESS
                                                                                                                                                                                                                                                                                                                                                                                                                       569 I--SDGGNW---IIKGT----ASGNSRGHFGASASVGYQW 599
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42;

Indels 268;

1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60

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Job time: 454 sec

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A:Status: preliminary
A:Status: DNA
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-1005 <582>
A:Cross-references: GB:AE005174; NID:g12514546; PIDN:AAG55766.1; GSPDB:GN00145; UWGP:Z16
A:Cross-references: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: Z1211; Z1651
                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                 61 EPVVRSALVLOFMIDKEGNGENESTGNIGWSIYYDNH---NTLHGATVT--LKAGDNLKI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- NAGN-NI 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        436 EITRNGKNIDI-----ATSMTPQFS-SVSLGAGADAPTLSVDDKGALNVGSKDANK--- 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       486 PVRITNVAPG-----VKEGDVTNVAQLKGVAQNLNNRI------DNVDGNARAGIAQAI 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                677 PLYTSMLTQAMDYDRILAGSRSHQTGVNGENNSVRLSIQGGHLGHDNNGGIARGATPESS 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 ATAG------LVQAYLPGKSMM----AIG------GGTYRGEAGYAIGYSS 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 KONTN------KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGA---NGNKVNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                           TSDTKGLNFAKETAGTNGDTTVHLNGI-----GSTLTDTLLNTGATTNVTNDNVTDDKKK 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 RAASVKDVLN-----TYD 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 QGTAESTTINKNGRQIILFSGLARDTLIYAGGDQSVHGRALNTTLNGGYQYVHRDGLALN 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TV-----EFLSAD--TKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT----- 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------GKGKG---ENGSSTDEGEGLVTAKEVID-----AVNKAGWRMKTTTAN 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 GQTGQADKFETVTSGTNVTFASGK-------GTTATVSKDDQ-GNITVKY 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 D-----SKAVAG 406
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                              1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60
                                                                                                                                                              Query Match 7.5%; Score 228; DB 2; Length 1005; Best Local Similarity 22.0%; Pred. No. 0.00037; Matches 180; Conservative 102; Mismatches 270; Indels 268;
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                                                                                                                                                            Query Match
Best Local Similarity
A; Accession: B85663
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Search completed: July 3, 2002, 08:12:32

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us-09-771-382-6.std.rsp

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 3, 2002, 08:30:09; Search time 48.34 Seconds (without alignments) 479.789 Million cell updates/sec Run on:

US-09-771-382-6 3060 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 599 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt\_40:\* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rickettsia	escherichia	escherichia	escherichia	rickettsia	r outer mem	r outer mem		campylobact		proteus mir		r outer mem	caenorhabdi	_	salmonella	ij	r outer mem	r outer mem	ŝ			_	listeria se	rattus norv	escherichia	haemophilus	_	bacteriopha	_	pseudomonas	pseudomonas	haemophilus
	scri	P15921	P39180	P32051	003155	2657	6869	<b>09kka</b> 3	3666	5827	5320	6466	P18127	053047	4487	P52143	5927	4914	053020	6653	098800	P38536	9624	7833	001838	_	P04949	P44969	P45384	P13390	5828	190	347	5354
	De	P1	P3	P3	ô	05	P9	60	P3	P3	Pl	P1	P1	05	P3	P5	P2	P1	05	00	00	P3	00	8	00	ô	PO	P4	P4	P1	Р3	03	03:	P4
SUMMARIES	DI	OMPA_RICRI	AG43_ECOLI	YDEK_ECOLI	AIDA_ECOLI		OMPB_RICTY	OMPB_RICCN	YDBA_ECOLI	SLAP_CAMFE	HLYA_SERMA	HLYA_PROMI	ICEN_XANCT	OMPB_RICRI	YMJB_CAEEL	YPJA_ECOLI	BIGA_SALTY	120K_RICRI	OMPB_RICPR	OMPB_RICJA	FLIC_SHIFL	APU_THETU	YS89_CAEEL	WAPA_BACSU	P60_LISSE	SP1_RAT	FLIC_ECOLI	IGAO_HAEIN	IGA2_HAEIN	VLTF_BPT5	- 1	ICEK_PSESX	ICEV_PSESX	HXA2_HAEIN
	DB	-	-	~	-	-	Η,	Н	٦	Н	-	-	٦	٦	-		-	-		-	-	-	٦	-	Н	-	Н	Н	Н	-	-	-	П	-
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de	Query Match	7.						6.5	•		6.2	•				•		•			•	•		•					5.5	•	•	5.4	5.4	5.4
	Score	241	240	228	225.5	221.5	200	199.5	σ	S.	189.5	8	æ	8	8	180	179	178.5	177.5	177.5	176.5			^	^	17	70.	68.	•	67.	167	9	٦,	164.5
	Result No.	-	7	e	4	ហ	9	7	œ	O	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q9pjt6 chlamydia m O84462 chlamydia t	P06620 pseudomonas P37710 enterococcu	Q9rb65 chlamydia p	P56867 deinococcus	Q02629 saccharomyc	P13126 deinococcus	P09815 pseudomonas		084419 chlamydia t	P20469 pantoea ana
Y741_CHLMU Y456_CHLTR	ICEN_PSESY ALYS_ENTFA	PM10_CHLPN	HPI1_DEIRA	N100_YEAST	HPI2_DEIRA	ICEN_PSEFL	FLA2_CAMJE	PMPC_CHLTR	ICEA_PANAN
		Н	Н	٦	٦	П	Н	7	7
1007	1200 671	928	948	959	1036	1210	575	1770	1322
5.4	5.2	5.3	5.2	5.2	5.2	5.3	5.2	5.2	5.2
164 162,5	161 160.5	160	160	160	159.5	159	158.5	158.5	158
3.4 3.5	36 37	38	33	40	41	42	43	44	4 5

## ALIGNMENTS

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STRAIN=ML 308-225;
Henderson I.R., Ow
                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 53-63.
                                                                                        Gregor J., Davis
Mau B., Shao Y.;
                                                                                                                                                                                                                      STRAIN-K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENE NAME
                                                                                                                                                                                              SEQUENCE
  RRARAR RR
                                                                                                                                                      34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1033 VGAGLLQVQGGVVKANTINLTDNASAVTFTNPVVVTGAIDNTGNANNGI-VTFTGNSTVT 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1202 LEFNGPLDGGGKAIPYYFKGAIANGNNAILNVNTKLLTASHLTIGTVAEINIGAGNLFTI 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KRTEVKIGAKTSVIKEKDGKLVTG----KGKGENGSSTDEGEGLVTAK----EVIDAVN 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VKEGDVTNVAQLKGVAQNLNNR-----IDNVDGNARAGIAQAIATAGLVQAYLPG-- 545
                                                                                                                                                                                                                                          DSTGNANNGIVTFTGNSTVTGDIGNTNALATVNVGAGTATLGGAVIKATTTKLTNAASVL 762
                                                                                                                                                      Gaps
                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                           NSALNAWVAVSELTRNHT-----KRASATVKT-AVLATLLFATVQANATDEDEEEELE
                                                                                                                                                                                                                                                                                  PVVRSALVLQFMIDKEGNGEN------ESTGNIGWSIYYDNHNTLHGATVTLKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNV - - - TDDKKKRAASVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --LNLNGALSQVTGD-----IGNTNSLATISVGAGTATLGGAVIKATTTKLTNAASVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVLNAGWNIKGVKPGTTASDNVDFVHTYDTVEFLSADTKTT----TVNVESKD---NG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  973 IKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFTGNSTVTGNVGNTNALATVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KA-----GWRMKTTTAN-------GQTGQADKFETVTSGTNVTFASGKGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1092 GNV----GNTNALATVNVGAGLLQVQGGVVKANTINLTDNASAVTFTNPVVVTGAIDNT
                                                                                                                                                                                                                                                                                                                                                                    ---- DNLKIKQNTNKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDT
                                                                                                                                                                                                                                                                                                                                                                                                            815 TATLGGAVIKATTTKLTNA---ASVLT-----LTNANAVLTGAVDNTTGGDNVGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNG----KNIDIATSMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PQFSSVSLGAGADAP----TLSVDDKGALNVGSKDANK-----PVRITNVAPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                        7.9%; Score 241; DB 1; Length 2249;
23.9%; Pred. No. 0.00014;
ive 72; Mismatches 275; Indels 178;
  M (TYPE II).
TYPE I (INCOMPLETE).
MW; A9D6646C089DF087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG43_ECOLI STANDARD; PRT; 1039 AA. P39180; P76360; P75614; P97241; Q46771; 01-FEB-1995 (Rel. 31, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Antigen 43 precursor (AG43) (Fluffing protein). FLU OR B2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : | | | : : | | | | | EGTVVFNGGVNGLNVGSNVAGTARNIGDGG 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            546 KSMMAIGGGTYRGEAGYAIGYS--SISDGG 573
1094 1165
1166 1180
2249 AA; 224333
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                                                                                                          Query Match
Best Local Simi
Matches 165;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rullication and N-terminal sequence of the alpha subunit of antigen 43, a unique protein complex associated with the outer membrane of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Misobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;

Yamamoto Y., Horiuchi T.;

A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97257509; PubMed-9103983;
Henderson I.R., Meehan M., Owen P.;
"Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
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FEMS Microbiol. Lett. 149:115-120(1997).
-1- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION.
FUNCTION AS AN ADHESIN.
THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
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SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
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EMBL; D90838; BAA15825.1; ALT_INIT.
EMBL; D90839; BAA15832.1; ALT_INIT.
EMBL; U24429; AAB47869.1; -.
ECOGENE; EG12686; flu.
Outer membrane; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caffrey P., Owen P.;
"Purification and N-terminal sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 171:3634-3640(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ML 308-225;
MEDLINE-89291704; PubMed-2661530;
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MEDLINE=97443975; PubMed=9298646;
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Submitted (JAN-1997) to t
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500 LTVSNTTLTQKAVNL---NEGTLTLNDSTVTTDVIAQRGTALKLTGSTVLNGAIDPTNVT 556
             AGIAQAIATAGLVQAYLPGKSMMAIGGGT-----YRGEAGYAIGYS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D90793; BAA15190.1; ALT_INIT.
D90794; BAA15197.1; ALT_INIT.
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                                                                                 557 LASGATWNIPDNATVQS 573
                                                           ISDGGNWIIKGTASGNS
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STRAIN-K12 / MG1655;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 TNKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 NEANTG-----GLQ-RVNPGGS 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSSTDEGEGLVTAKEVIDAVN---KAGWRMKTTTANGQTG--QADKFETVT-SGTNVTFA 358
                   ANTIGEN 43 BETA CHAIN.

K -> N (IN STRAIN ML 308-225).

SL -> FF (IN STRAIN ML 308-225).

T -> K (IN STRAIN ML 308-225).

W -> L (IN STRAIN ML 308-225).

W -> L (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

B -> V (IN STRAIN ML 308-225).

C -> K (IN STRAIN ML 308-225).

C -> S -> P (IN STRAIN ML 308-225).

C -> S -> P (IN STRAIN ML 308-225).

C -> S -> P (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 ISGNVSPSK----GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 VSGTRSDGKAFSIGGGOADALMLEKGSSFTLNAG----DTATDTTVNGGLFTARGGTLAG
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6.4e-05;
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STRAIN ML 308-225).
STRAIN ML 308-225).
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5170D647C8DEEBE0 CRC64;
            ALPHA CHAIN.
         ANTIGEN 43 ALPHA CHAIN.
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S -> T (IN S
Q -> L (IN S
S -> I (IN S
ETV -> TTT (
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21.9%; Pred. No. 6.
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888 88
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61 6
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Matches 148; Conserv
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STRAIN-KIS.

Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,

Rasal H., Rashimoto K., Kitakawa M.,

Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,

Makano S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,

Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horluchi T.;

A 570-kb DNA sequence of the Escherichia coli K-12 genome

corresponding to the 28 0-40.1 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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-!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                 Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
YDEK_ECOLI STANDARD; PRT; 1325 AA. P32051; P705140; P77168; O1-0771993 (Rel. 27, Greated) O1-NOV-1997 (Rel. 35, Last sequence update) 16-OGT-2001 (Rel. 40, Last annotation update) Hypothetical lipoprotein ydek precursor (ORFT). YDEK OR ORFT OR B1510.
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                                                                                                                                                                                                                                                               EPVVRSALVLQFMIDKEGNG-----ENESTGNIGWSIYYDNHNTLHG----ATVTLKA 109
                                                                                                                                                                                                                                                                                                            GDNLKIKONT -----NKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNI - 162
                                                                                                                                                                                                                                                                                                                                                          163 TSDTKGLN-----FAKETAGTNGDTTVHLNGIGSTLTDTLLNTGA----TTNVTN 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 WRMKTTTANGOTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVK-YD-VNVGDA 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LN--VNQLQNSGWNL------DSKAVAGSSGKVISGNVSPSKGKMDETVN 428
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                                                                     POTENTIAL.
HYPOTHETICAL LIPOPROTEIN YDEK.
N-ACYL DIGITCERIDE (POTENTIAL).
N -> K (IN REF. 3).
N -> S (IN REF. 3).
M -> S (IN REF. 3).
                                                                                                                                                                  7.5%; Score 228; DB 1; Length 1325; 23.1%; Pred. No. 0.00033; ive 72; Mismatches 257; Indels 171
EMBL, X73295; CAA51730.1; ALT_FRAME.
PIR; S34315; S34315.
Eccogene; EG11780; ydeK.
PROSITE: PS001013; PROKAR_LIPOPROFIEIN; 1.
Hypothetical protein; Membrane; Lipoprotein; Signal;
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01-JUN-1994 (Rel. 29, Last sequence update)
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Q03155;
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                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.

STRAIN=2787 (0126:H27);

MEDLINE=92326638; PubMed=1625582;

MEDLINE=92326638; M.A.;

"AIDA-I, the adhesin involved in diffuse adherence of the diarrheagenic Escherichia coli strain 2787 (0126:H27), is synthesized via a precursor molecule.";

Mol. Microbiol. 6:1539-1546(1992)

-!- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI TO EPITHELIAL CELLS.
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Enterobacteriaceae;
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PIR; S28634; S28634.
Cell adhesion; Signal; Outer membrane; Plasmid.
   Proteobacteria; gamma subdivision;
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                                                                                                                                                                                                                                                                                                                                          STRAIN=Malish 7;
MEDLINE-94171067; PubMed-8125327;
Crocquet. Valdes P.A., Weiss K., Walker D.H.;
"Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
Gene 140:115-119(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Indian tick typhus, MI, Malish 7, and Moroccan; MEDLINE=97015921; PubMed=8862558; Roux V., Fournier P.E., Raoult D.; "Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rOmpA."; Clin. Microbiol. 34:2058-2065(1996).
                      --VGS 480
                                        AVWSMFPGTASGA-----NVNLSGRLNAFAGNVVGTILNQEGRQYVYSGATATSTVGN 549
                                                             481 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARA-----GIAQAIAT 535
                                                                          437 IVNTSGFQRINSGGTAPVQNSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRGIWYSNFLT 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ø
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
                                                                                                                                                                         ODPA_RICCN STANDARD; PRT; 2021 AA. 052668; Q52669; Q52657; P95591; P95592; P95594; Q52667; Q52668; Q52669; Q52670; Q52674; Q6272-2001 (Rel. 40, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Quter membrane protein A precursor (190 kDa antigen) (Cell surface annigen) (rOmp A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: GLYCOSYLATED (BY SIMILARITY). SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=781;
                                                                                                        536 AGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGN 574
                                                                                                                    SMTPQFSSVSLGAGADAPTLSVDDKGALN-
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21442074; Pubmed=11557893;
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MISSING (IN STRAIN MAI).

MISSING (IN STRAIN MOROCCAN).

MISSING (IN STRAIN MOROCCAN).

T -> II (IN STRAIN INDIAN TICK TYPHUS).

D -> A (IN STRAINS INDIAN TICK TYPHUS, MI
AND MOROCCAN).
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M -> I (IN STRAIN INDIAN TICK TYPHUS).
D -> K (IN REF. 1).
I -> V (IN REF. 1).
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KATLGGAIIKATTTK -> LLQVQGGVVKANTIN (IN
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N -> D (IN REF. 1).
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22.6%; Pred. No. 0.0011;
live 83; Mismatches 264;
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  modified and this statement is not remoentities requires a license agreement (or send an email to license@isb-sib.ch)
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Pfam; PF02708; rOmpA_rOmpB; 1.
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U45244, AAB49566.1;
U43418, AAA8666.1;
U83440, AAC35176.1;
U83443, AAC35179.1;
U83448, AAC35189.1;
U83453, AAC35189.1;
                                                                                                               EMBL; U01028; AAA17405.1; -.
                                                                                                                                         AE008674; AAL03811.1;
U43794; AAB49549.1; -.
U43798; AAB49550.1; -.
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| 1044 NAQDIHFRALDSALVLSNLTGVGVNNILLAADLVAPGVDEGTVVFDGGVNGLNIGSNVA- 1102
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15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rômpB)
(rômp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94040787; PubMed=8224886;
Habhn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene encoding the crystalline
surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
VRSALVLQFMIDKEGN-----GENESTGNIGWSIYYDNHNTLHGATVTLKAG----
                                                                ----VAPGVKEGDV-----TNVAQ
                       VVTG-----AIDNTGNANNGIVTFTGDSTVTGNIG-----NTNAL--ATISVGAGKATL
                                                111 DNLKIKQNTNKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLN
                                                                                                 171 FAKETAGTINGDTTVHLINGIGSTLTDTLLINTGATTINVTINDNVTDDKKKRAASVKDVLINAGW
                                                                                                                          643 VTGNIGNTNALATVNV-GAGIATLEGAVIKATTTKLTN------AASVLTLTNVNA
                                                                                                                                                   231 NIKGVKPGTTASDNVDFVHTYDTVEFLSADTKTT----TVNV---ESKDNG---KRTEVK
                                                                                                                                                                                                    281 IGAKTSVIKEKDGKLVTG----KGKGENGSSTDEGEGLVTAK----EVIDAVNKA----
                                                                                                                                                                                                                                                                             812 VQGGVVKSNTINLTDNASAVTFTNPVVVTGAIDNTGNANNGIVTFTGDSTVTGNIGNTNA
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Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                      --GWRMKTTTAN------
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SEQUENCE FROM N.A.
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or send an email to license@isb-sib.ch)
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                                     Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody binding sites on CNBr fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KPGTTASDNVDFVHTYDTVEFLSADTKTTTVNVESKD------NGKRTEVKI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Pred. No. 0.01;
86; Mismatches 256; Indels 248;
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32 KDA BETA PEPTIDE.
MEMBRANE ANCHOR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      S-LAYER WITH HEXAGONAL SYMMETRY.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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V -> I (IN REF. 2).
G -> A (IN REF. 2).
G -> S (IN REF. 2).
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0.01;
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                  MEDLINE=92114896; PubMed=1370573;
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Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                                                                      Mol. Immunol. 29:95-105(1992).
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STRAIN-WILMINGTON;
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Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia
australis, the most divergent rickettsia of the spotted fever group.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: THE 12D KDA SUBFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
                                                                                                                                                                                                                                                                 ---DFGNLAVQIVVPNNKILTGNFIGDA-----KNNG-NTAGVITFNANGTLVSGNTDP 450
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GGNLKGVIEFDTTAAAGKLIANGGAANAVIGTDNGAGRAAGFIVSVDNGNAATISGQVYA 352
                                                                 318 KEVIDAVNKAGWRMKTTTANGQT------GQADKFETVTSGTNVTFASGKGTTATV 367
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
02-MAR-2002 (Rel. 50, Last annotation update)
03-MAR-2002 (Rel. 50, Last annotation)
04-MAR-2002 (Rel. 50, Last annotation)
05-MAR-2002 (Rel. 50, Last annotation)
05-MAR-2002 (Rel. 50, Last annotation)
06-MAR-2002 (Rel. 50, Last annotation)
07-MAR-2002 (Rel. 50, Last annotation)
07-
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                                                                                                                                                                                                368 SKDDQGNITVKYDVN-----VGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP
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                                                                                                                               353 KDIV-----IQSANAGGQVTFEHLVDVGLGGKTNFKTADSKVIITENASFGST---
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Rickettsiaceae; Rickettsieae; Rickettsia.
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Samson D., Roux V., Cossart P., Weissenbach J., Claverie J
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MEDLINE=21442074; PubMed=11557893;
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                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 DNHNTL----HGATVTLKAGDNLKIKQNTNK----NTNENTNDSSFTYSLKKDLTDLTSV 146
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                                                                                                                                                                                                                                                                                                                                                                                                               P -> A (IN STRAIN INDIAN TICK TYPHUS).

G -> S (IN STRAIN INDIAN TICK TYPHUS).

V -> A (IN STRAIN INDIAN TICK TYPHUS).

N -> D (IN STRAIN INDIAN TICK TYPHUS).

I -> V (IN STRAIN INDIAN TICK TYPHUS).

A -> T (IN STRAIN INDIAN TICK TYPHUS).

R -> L (IN STRAIN INDIAN TICK TYPHUS).

KD -> GH (IN REF. 3).
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                             FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 NGDTT----VHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKD---VLNAGWN
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                                                                BACTERIUM IS COVERED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1655;
                                                                                                                                                                                                                                                                                                                                                                                  120 KDA SÜRFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
                                                                                               SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E49E19377D5FCE37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.5%; Score 199.5; DB 1;
23.6%; Pred. No. 0.011;
Live 66; Mismatches 253;
                                             (BY SIMILARITY).
SUBCELLULAR LOCATION: CELL WALL. THIS BACTERI
LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY)
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E -> D (IN F
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EMBL, AF123726; AAF34129.1; --
EMBL; AF149110; AAD39533.1; --
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
Antigen; S-layer; Cell wall; Complete
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Misobuchi K., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Taqami H., Takeda J., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., Saito N., A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28 0-40.1 min region on the linkage map.";
431 -AGNN--IEITRNGKNIDIATSMTPQ----FSSV----SLGAGADAPTLSVDDKGALNV 478
                                            VIGNNGAVQFAHNTYLITRTTNAAGQGKIIFNPVVNNNTTLATGTNLGS-ATNPLAEINF 706
                                                                                             GSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDG-NARAGIAQAIATAG 537
                                                                                                                                            GSKGAANVDTVLNVGKGVNL-YATNITTTDA---NVGSFIFNAGGTNIVSG-----TVG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SIMILARITY: TO S.TYPHIMÜRIUM ORF NEAR CYSG (AC P25928).
-:- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMIO ACIDS 839 AND 840.
                                                                                                                                                                                                                             GQQGNKFNTVALDNGTTVKFLGNATFNGNTTIAAN-STLQIGGNYTADFVASADGTG 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=KI2 / MG1655;
MEDLINE-97426617; PubMed=9278503;
MEDLINE-97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moszer I., Glaser P., Danchin A.; "Multiple IS insertion sequences near the replication terminus in Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                              538 LVQ-----AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRG
                                                                                                                                                                                                                                                                                                                                                                     YDBA_ECOLI STANDARD; PRT; 2003 AA. p1366; P76087; P76088; P76086; P76859; P76859; P76088; P76088; P76859; P76088; P76088; P76859; P76088; P76088; P76088; P76085; P76859; P76085; P76081; P760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000237; AAC74483.1; ALT_SEO.
EMBL; AE000237; AAC74487.1; ALT_SEO.
EMBL; D90778; BAA15009.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97251357; PubMed-9097039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92190338; PubMed=1665988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 464-2003 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochimie 73:1361-1374(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDD-----QGN 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        716 DSEVTSROSNLFDGSAE-----KTSGLVVIGDGNTVNMNGGLELIGEKNALADGSQVT 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIYYDNHNTLHGATVTLKAGDNLKIKQNTNKNTNENTNDSSFTYSLKKDLTDLTSVETEK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 INGDDATANNNGKTTVDGKDSTGTEINGNNGKVIQDGDLDVSGGGHGIDITGDSATVD-N 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGTMTVTDPESIGIQVDG-DQAVVNNEGESAITNGGTGTQINGDDATANNNGKTTVDGKD 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 ITVKYDVNVGDALNV----NQLQNSGWN--LDSK-----AVAGSSGKVISGNVSPSKGKM 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DETVNINAGNNIEITRNGKNIDIATSM-TPQFSS-VSLGAGADAPTLSVDD-----KG 474
                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      33 TVKTAVLATLLFA-TVQANATDEDEEEELEPVVRSALVLQFMIDKEGNG-ENESTGNIGW 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         475 ALNVGSKDANKPVRIT-----NVA-----PGV-----KEGDVTNVAQLKGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 TEKTLTIRDSVFTYTENADGTISLQDSN----GRKATINLWQIDEANNTVALEGVSADGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 TKWQYNHN---GELVI--TGDNATV--NNNGKTTVDGKDSTGT---EINGNNGKVIQDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658 GINV-SGDAN-TVNITGNVLVDKDKTADNAAEYFFDPSVGINVYGSDNNVTLDGKLTVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QN-LNNRIDNV-DGNARAGIAQAIATAGLV-------QNYLPGKSMMAIGGGTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- LNFAKETAGINGDITVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDVSGGGHGIDITGDSATVDNKGTMTVTDPESMGIQIDGDKAIVNNEGESTITNGGTGTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DQAIVNNEG----ESTITNGGTG----TQINGNDAT-ANNSGKTTVDGKDSTGTKIAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 KRAASVKDVLNAGWNIKGVKPGTTASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGK-
                                                                                                                                                                                                                                                                                                                                             185;
                                                                                                                                                                                                                                                                                 Length 2003;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                       I -> V (IN REF. 2).
I -> V (IN REF. 2).
W; B83A12C8B5322OEE CRC64;
                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                    6.5%; Score 197.5; DB 1;
24.2%; Pred. No. 0.017;
ive 89; Mismatches 249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
S-layer protein (Surface array protein) (SAP)
SAPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             933 AA
                                                                                                            Hypothetical protein; Complete proteome CONFLICT 489 I -> V (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RGEAGYAI -----GYSSISDGGNWIIKG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLRTGYSYTSVIVVSGESSVYLNGDTTISG 798
EMBL, D90778; BAA18880.1; ALT_SEQ. EMBL, D90779; BAA18881.1; ALT_SEQ. EMBL, SC2680; -; NOT_ANNOTATED_CDS. EcoGene; EG11307; ydba.
                                                                                                                                                                                                205949 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSFGANGNKVNITSDT----KG-
                                                                                                                                                                                                                                                                                                                  Best Local Similarity 24.23
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                        495
                                                                                                                                                                     495 49
2003 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLAP_CAMFE
P35827;
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663 ASGGELSVESKTGNINVKAAERQQNIDEQKTALTVNGYAKEAGDKQYRAGLRIEHTRDSE 722
                                                                                            ---DVTALMIVVKIVLDAAAKD-----TNIALGTAAADKALVIDTGIETLNITSLVKA 721
                                                        508 ---KGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMOLYSIN.
W; D669B476FE7DAD51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 GNGENESTGN---IGWSIYYDNHNTL----HGATVT----LKAG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2%; Score 189.5; DB 1;
22.3%; Pred. No. 0.033;
Live 68; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            PRT; 1608 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1608 AA; 165078 MW;
                                                                                                                                                            565 GYSSISDGGNWIIKGTASGNS 585
                                                                                                                                                                                        |:|: | | ||| : :|
778 DASAITLGANATIKGGSGADS 798
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Best Local Similarity 22.3#
Matches 138; Conservative
                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serratia marcescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=615;
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                                                                                                                                                                                                                                                                                                                                            HLYA_SERMA
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ALLYA_SERMA
ALLYA_SERMA
DT P11-NDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch/ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : |:|:| | : |: | | |:| | 331 GTGKVDVVAGKISALTADSRTSVNLTATNDTITLTSANAATSVNLKQRQAKD-----AT 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222 VKDVLNAGWNIKGVKPGT----TASDNVDFVH-------TYDTVEFLSA-D 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : : | | | : | | 385 ITSAMQQKYNNRRNRIATITSATAVENLTVKHATNVALNGGMDKLATVTLDNAALTAAID 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 TKT-TTVN-VESKDNG-----DGKL 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 VIGKGKGENGSSTDEGEG---LVTAKEVIDAVNKAGWRMKTTTTAN-----GQTGQADK 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 FETVTSGTNVTFASGKGTTATVSK -- DDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404 VAG---SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 GNGTNKSTLSAFDKTRWSVL--GRDTLNAIFTAITRAALLTDQAELIITKRRTNVENIN- 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 SSFTYSLKKDLT---DLTSVETEKLSFGANGNKVNITSD-TKGLNFAKETAGT----- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 -------NGDTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAAS 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619 VATADLSSSAFKNSVIITTKEAADTTLTINKDQVI-----NFTAADAGSVKLITVKLN 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            461 AGADAPTLSVDDKGALNVGSKDANKPVRITNVAPGVKEGD------VTNVAQL--- 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 GNGENEST----GNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQN---TNKNTN-ENTND 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                       MEDLINE-91035477; PubMed-2229082; Blaser M.J., Gotschlich E.C.; J. Biol. Chem. 265:19372-19372(1990).
-!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS CRITICAL FOR VIRULENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=84-32 / 23D;
MEDLINE=90354448; PubMed=2387868;
Blaser M.J.; Gotschilch E.C.;
"Surface array protein of Campylobacter fetus. Cloning and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F88C729B4BA5B1E9 CRC64;
                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
                                                                                                                                                                                                                                                                 Biol. Chem. 265:14529-14535(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wall; S-layer.
ENCE 933 AA; 96757 MW;
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Best Local Similarity 22.79
Matches 141; Conservative
                                                      NCBI_TaxID=196;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                     MEDIINE-88257037; PubMed-3290200;
Poole K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                           J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 ANGNKVNITSDTKGLNFAKETAGTNGD----TTVHLNGIGSTLTDTLLNTGATTNVTNDNV
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 195;
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ICEN_XANCT P18127;
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                                                                                                                                                                                                                                                         119;
                                                                                                                                        SEQUENCE
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Best Local 9
                                                                                          SIGNAL
                                                                                                                     CHAIN
                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LOCATION: Outer membrane.
-:- MISCELLARBOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSTBLE FOR PORE FORMATION.
-:- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
212 TDDKKKRAAS------VKDVLNAGWNIKGVKPGTTASDNVDFVHTYDTVEFLSAD 260
                                                                                                                                                                                       321 IDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVKYD 380
                                                                                                                                                                                                                                                                                                                                                                            GKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKG-----ALNVGSKDANKPVRITN-- 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     940 AVVSSVQAGSIDINAKGEVRDQGTQYQASKG-AVNLTADSHRSEAAANRQDEQSRDTR-- 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
                                              ---KVSFLAAD
                                                                                          TKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEV
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                                           723 KTTRTENSASSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGN----
                                                                                                                                                                                                                                --GIDKLGSGVEAGYENNKT-QAQSSKAITSGSDV-----
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Last sequence update)
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STRAIN=ISOLATE 477-12;
MEDLINE=90170827; PubMed=2407716;
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01-AUG-1990 (Rel. 15,
01-NOV-1990 (Rel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               319 EVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVS--KDDQGNIT 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            803 VTKNRGSQTEVAGDLTITANKDLLHEGASHHVEGRYQESGENIQHLAVNDSETSKTDSLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETEKLSFGANGNKVNIT-SDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLLNTGATTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 VKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   750 ITGD-NVAFVSTENKKQTD--NTDTTISGGFS---YTGGVDKVGSKADFQYD-KQHTQTE
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Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                       161;
                                                                                                                                                                                                                               Length 1577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation gene inaX from "Conserved repetition" \ensuremath{\mathsf{Cons}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        524 NARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDG 572
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                                                                                                                  30 1577 HEMOLYSIN.
1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                       225;
                                                                                                                                                                                                                                                                                                                                               73 MIDKEGNGENESTGNI-----GWSIYYDNH--NTLHGATVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              --LKAGDNLKI--KQNTNKNTNENTNDSSFT-----
                                                                                                                                                                                                                            6.1%; Score 187.5; DE 20.2%; Pred. No. 0.04; tive 84; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1567
                                                          Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=X56S;
MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                920 TPNVGVEVGIK------
EMBL; M30186; AAA25657.1;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ice nucleation protein.
                                                                                                                                                                                                                                                            Similarity
                                PIR; A35140; A35140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=343;
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7 IIWNSALNAWVAVSELTR------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; S-layer; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Matches 178; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Microbiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=783;
                                                                                                                                                                                                                                                                         OMPB_RICRI
Q53047;
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SEQUENCE
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                                                                                                                                                                                                                                             OMPB_RICRI
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                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            962 GTAGADSTLIAGYGSTQTSGS-----DSSLTAGYGSTQTAREGSDVTAGYG 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1008 STGTAGADSTLIAGYGSTQTAGSD--SSLTAGY----GSTQTARQGSDVTAGYGSTGTAG 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1062 ADSTLIAGYGSTQTAGSDSSLIAGYGST-QTARQGSDI-----TAGYGSTGT-AGADSS 1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1114 LIA--GYGSTQTAGYDSNLTAGYGSTQTAREDSSLTAGYGSTSTAGHDSSLIAGYGSTQT 1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 VIKEKDGKLVTGKGKGENGSSTDEGECLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKF 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 AGIAQAIATA-GLVQAYLPGKSMMAIGGGTYRGEAGY----AIGYSSISDGG--NWIIKG 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           712 SDVTAGYGSTGTAGADSTLIAG--YGSTQTSGSD------SSLTAGYGSTQTAR 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 EGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTNKNTNENTNDSSFTYSL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       758 KGSDVTAGYGSTGTA------GADSTLIAGYG------STQTSGSDSSLTAGY 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 KKDLT-----DLTSVETEKLSFGA-------NGNKVNITSDTKGLNFAKE---- 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ----TAGTNGDTTVHLNGIGSTLT---DTLLNTGATTNVTNDNVTDDKKKRAASVKDVL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 SELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEELEPVVRSALVLQF---MIDK 76
                                                                                                SUBCELGULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
OCTAMPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 NAGWNIKGVKPGTTASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        859 TAGYGSTGTAGADSTLISGYGSTQTAGSDSSLTAGYGSTQTARKGSD-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLSVDDKGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNAR
                                                     ENABLE BACTERIA TO NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799 GSTQTARKGSDITAGYGSTGTAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTAREGSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 907 TAGYGSTG----TAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTARKGSDMTAGYGST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.1%; Score 185.5; DB 1; 19.8%; Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Mismatches
                      MOI. Gen. Genet. 223:163-166(1990).
-!- FUNCTION: ICE NUCLEATION PROTEINS ENAI
CRYSTALLIZATION IN SUPERCOOLED WATER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00314; ICE_NUCLEATION; 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00818; Ice_nucleation; 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000258; Ice_nucleatn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00327; ICENUCLEATN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X52970; CAA37140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; S11672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P06620; 11NA
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NAME OF THE PROPERTY OF THE PR
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30-MAY-2000 (Rel. 39, Last sequence update)
16-CT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NHTKRASATVKTAVLATLLFATVQANAT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92167802; PubMed=1724278; Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsia is encoded by an unusually long open reading frame:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gilmore R.D. Jr., Joste N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encodi
120 kb surface-exposed protein of Rickettsia rickettsii.";
Mol. Microbiol. 3:1579-1586(1989).
-i- FUNCTION: THE 120 kba SURFACE-EXPOSED PROTEIN IS A MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 KDA SURFACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia rickettsii.
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evidence for protein processing from a large precursor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D7AB70FB7087F618 CRC64;
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22.9%; Pred. No. 0.053;
ive 83; Mismatches 264;
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                                                                                                                                                                                                                                                                                                                            1654 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5:2361-2370(1991).
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MEDLINE=90136087; PubMed=2515418;
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InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                            580 TASGNSRGH-----FGASASVGYQ
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1654 AA; 168184 MW;
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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MEDLINE-94150718; PubMed-7906398;
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Garden A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DAKKTLTLGGANIIGAGGTIDLQANGGTIKLT-STQNNIVVDFDLAIATDQTGVVD
 ---IYYDNHNTLHG
                    APLIL -- GDNAVIANGVNGTLNVTNGFIQVSNKSFATVKAINIADGQGIIFNTDANNANT
                                                                                                                                ----IGSTL
                                                                                                                                                            --LNLQAGGTTINFTGTDGTGRLVLLSKHAAATNFNITGSLGGNLKGVIEFNTVAVDGQL
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                                                                                                                                                                                                TDTLLNTGATTNVTNDN------VTDDKKKRA-----ASVKDVLNAGWNIKGV---
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                                                                 TDLTSVET
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01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 96.6 kDa protein F59B2.12 in chromosome III.
DEDEEEELEPVVRSALVLQF - - - - MIDKEGNGENESTGNIGWS - -
                                                                                                                               EKLSFGANGNKVNIT-SDTKG--LNFAKETAGTNGDTTVHLNG-
                                                               ATVTLKAGDNLKIKQNTNKN---TNENTNDSSFTYSLKKDL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RTEVKIGAKTSV-----IKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDA--VNKA 327
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   Saunders D., Shownkeen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              328 GTSSMEASHAGSNSSKINSASGQSSDLSWVGPNGIKSHSTSNKTDNYALDEANQSAGSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 ITSDTKGLNFAKETAG-TNGDTTVHLNGIGSTLTD-----TLLNTGATTNVTNDNVTDDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 VKYDVNVGDALNVNQLQNSGWNLDSK - - AVAGSSGKV - ISGNVSPSKGKMDETVNINAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              388 EQIGKNGORSLNESSIE-SGRKAESRNNTAADTLDSVDANGTVSSSHSKSASGTSLDENH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOSRSAALDEGNEFVNOQNADGTFLRNNTGHKNTDEHLSHNVLDENAQMSIGADGTSHNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216 KKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 TNRKGSVGDSHNA-----ASD----AHS----NFESLDAQG---NKKSQNYSK
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                                                                                                                                                                                                                                                                                                                                                                                                                    Score 180.5; DB 1; Leuy...
Pred. No. 0.047;
...marches 227; Indels 107;
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownk Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                               E464FD86B14945DE CRC64;
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P52143; P76610; P77017; P77019;
                                                                                                                                                                                                                                                                                                                         PIR, S31132, S31132.
WormPep, F5982.12, CE01024.
Wypothetical protein.
SEQUENCE 918 AA; 96560 MW;
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                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                           Wohldman P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Construction of a contiguous 874-kb sequence of the Escherichia coli - K12 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";

DNA Res. 4:91-113(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 IGSTLTDTLLNTGATTNVTNDNV-----TDDKKKRAASVKDVLNAGWNIKGVKPGT 239
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Itoh T., Kimura S., Kitaqawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Tachma T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12 / WG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 1569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ecodene: EG131313; ypjA.
Hypothetical protein; Outer membrane; Complete proteome.
SEOUENCE 1569 AA; 162774 MW; 0D006A9A32154596 CRC64;
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-!- SUBCELLULAR LOCATION: Outer membrane (Potential).
-!- SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.
01-OCT-1996 (Rel. 34, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical outer membrane protein ypjA.
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EMBL; AE000350; AAC75695.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      754 NEGGLAENSVLNDGGTLDVREK-------GSATGIQQSSQGALVATTRAT 796
                                    378 ------KYDV---NVGDALNVNQLQN--SGWNLDSKAVAGSS----GKVISGNVS
                                                                                                                                                                                         584 QQSGGALIASTTSG-----TLIEGTNSYGDAFYIRNSEAKNVVLENAGSLTVVTGS
                                                                                                                                                                                                                                                                                                                 635 RAVDTIINANGKMDVYGKDVGTVLNSAGTQTIYASATSDKANIKGGKQTVYGLATEANIE
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                                                                                                                          326 -KAGWRMKTTTANGQTGQADKFETVTSGTNV---TFASGKGTTATVSKDDQGNITV---
   ---VIDAVN---
   VIKEKDGKL-VTGKGKGENGSSTDEGEGLVTAKE----
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Search completed: July 3, 2002, 08:30:20 Job time: 1191 sec

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Q9ps7 neisseria m
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Q9ps7 neisseria m
Q9ps7 neisseria m
Q9ps4 neisseria m
Q9ps neisseria m
Q9ps neisseria m
Q9ps neisseria m
Q9js neisseria m
Q9f3x6 pasteurella
Q9f2d8 salmonella
Q9pc4 xylella fas
Q9f2d8 salmonella
Q9pd50 xylella fas
Q9f3x5 pasteurella
Q9pd63 xylella fas
Q9f647 rhizobium n
Q9hf2 rhizobium n
Q9hf2 rhizobium n
Q9lf47 escherichla
Q9lf48 escherichla
Q9se20 rhizobium n
Q9se20 rhizobium n
Q9se20 rhizobium l
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NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Hood D.W., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERAIN-H38;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.
Tdentification and characterization of a gene encoding a novel
membrane protein of Neisseria meningitidis.";
submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226383; AAF42532.1;
EMBL; AF157608; AAK68869.1;
SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    599 AA
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MEDLINE=20175756; PubMed=10710308; ...
                                                                                                                                   09J0W4
P71401
Q9F3X6
Q9F3X6
Q9F0X04
Q9FDX0
Q9FDX0
Q9F3X5
Q9PDX0
Q9RXQ7
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                                                            PRELIMINARY;
 Neisseria meningitidis.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                      MNKIYRIIMNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
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             Indels
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Science 287:1816-1820(2000).
EMBL; AF226382; AAF42531.1; -
SEQUENCE 598 AA; 62718 WW; 9095F8E31AD7C76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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NCBI_TaxID=487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                         DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Score 2832.5; DB 2;
Pred. No. 2.1e-111;
....trhes 28;
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Science 287:1816-1820(2000).
EMBL; AF226359; AAF42508.1; -.
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MEDLINE=20175756; PubMed=10710308;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                       membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF226381; AAF42530.1; -.
                                                                                                                                                                                    E6C7AEF0BB8A63CB CRC64;
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                                                                         Moxon R.,
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                                                                       Peak I.R., Srikhanta Y., Dieckelman M., "Identification and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-2001 (TrEMBLrel, 19, Created)
01-DEC-2001 (TrEMBLrel, 19, Last seq
01-DEC-2001 (TrEMBLrel, 19, Last anno
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 Science 287:1816-1820(2000)
                                      SEQUENCE FROM N.A.
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MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Battolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                              GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
                                                       Length
                                                                                            Indels
63A6A3BD7F0F2EE3 CRC64;
                                                   5;
                                              Score 2830.5; DB 2;
Pred. No. 2.5e-111;
3: Mismatches 29;
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62763 MW;
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598
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETRAIN-B2198, AND 297-0;
MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Scarlato V., Masignani V., Giuliani E., Capecchi B.,
Comanducci M., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
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                                                                                   Length 598;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TREMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN (SNA992 (NHHA OUTER MEMBRANE PROTEIN)
            a gene encoding a
                                                                                                        Indels
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin "Identification and characterization of a gene encoding membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI57603; AAK68864.1;
SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;
                                                                                    2;
                                                                                  Ouery Match 92.2%; Score 2821.5; DB 2; Best Local Similarity 92.7%; Pred. No. 6e-111; Matches 555; Conservative 13; Mismatches 30;
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Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter Moxon E.R., Grandi G., Rappuoll R.; Rappuoll R.; "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin Identification of haracterization of a gene encoding membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF22638; AAF42517.1;
EMBL; AF22638; AAF42507.1;
EMBL; AF25668; AAK68865.1;
EMBL; AF15604; AAK68865.1;
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; Pred. No. 3.7e-110;
12; Mismatches 28;
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Best Local Similarity 92.5%;
Matches 554; Conservative 1:
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Science 287:1816-1820(2000).
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                                                STRAIN=528, AND 1000;

X MEDLINE=20175756; PubMed=10710308;
A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Pizza M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
A Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
A Ratti G., Santini L., Savino S., Scarsalli M., Storni E., Zuo P.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffiles A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.,
Tidentification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
E. Science 287:1816-1820(2000).
REMBL; AF226356; AAF42509:1;
REMBL; AF226356; AAF42509:1;
                                                                                                                                                                                                                                                                                                                                                                 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAĞTNG 180
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           beta subdivision; Neisseriaceae; Neisseria
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                                                                                                                                                                                                                                    Length 595;
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                                                                                                                                                                                                      62120 MW; 8212C96380142BFC CRC64;
                                                                                                                                                                                                                                    91.2%; Score 2792; DB 2; 92.5%; Pred. No. 1e-109;
                                                                                                                                                                                                                                                         15; Mismatches
           Proteobacteria;
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Matches 556; Conservative
                                          SEQUENCE FROM N.A.
                   NCBI_TaxID-487;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                                                                                                                                                                                                                                                       Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
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"Identification of Vaccine Candidates Against Serogroup
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL, AF226311; AAF42520.1;
SEQUENCE 600 AA; 62762 MW; 36256963E0598CDI CRC64;
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Last annotation update)
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       Created)
                                                                                                                                                                                                                                                                                    MEDLINE=20175756; PubMed=10710308;
                                                                             OUTER MEMBRANE PROTEIN GNA992.
01-0CT-2000 (TrEMBLEL 15,
01-0CT-2000 (TrEMBLEL 15,
01-MAR-2001 (TrEMBLEL 16,
                          01-OCT-2000 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel.
                                                                                                                               Neisseria meningitidis.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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595 VGYQW 599

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121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG 180
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476 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQ 535
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Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing.";
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                           Length 594;
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SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last segu
01-MAR-2001 (TrEMBLrel. 16, Last anno
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MEDLINE=20175756; PubMed=10710308;
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X MEDINE=20175756; PubMed=10710308;

MEDINE=20175756; PubMed=10710308;

A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

A Comanducci M., Jennings G.T., Baldi L., Bartollni E., Capecchi B.,

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

M. Moxon B.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";

Science 287:1816-1820(2000).

E. Science 287:1816-1820(2000).

E. SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEDRRANE PROTEIN GNA992.
                                                                                      594 AA
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                                                                                     PRELIMINARY;
                                                                                                                                                                                         Neisseria meningitidis
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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                                               SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-EG327;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
Tidentification and characterization of a gene encoding a novel c
membrane protein of Neisseria meningitidis.";
Submitteed (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF157605; AAK68865.1; - .
SEQUENCE 594 AA, 62297 MW; 9DDD48B04B3A8EA2 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NHHA OUTER MEMBRANE PROTEIN.
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Best Local Similarity 91.7%
Matches 549; Conservative
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                                                                                                              Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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MEDLINE-20175756; PubMed=10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jannings G.T., Baldi L., Bartolini E., Capecchi B.,

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettellin H.,

Hood D.W., Jeffrites A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B
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                       291 GKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFAS
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                                                                                       541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN (GNA992.
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SEQUENCE 590 AA; 6166
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STRIN-NCP165, 90/18311, AND 93/4286;
STRIN-NCP165, 90/18311, AND 93/4286;
STRIN-NCP165, 90/18311, AND 93/4286;
STRIN-NCP165766; Pubmed-10710308;
A MEDLINE-20175766; Pubmed-10710308;
A Galectic C.L., Luzzi E., Manetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarsoli M., Storni E., Zuo P., Brocker M., Hundt E., Kanpp B., Blair E., Mason T., Tettelin H., A Moxon E.R., Grandi G., Rappuoll R.;
A Moxon E.R., Grandi G., Rappuoll R.;
Motor D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., A Moxon E.R., Grandi G., Rappuoll R.;
Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
E. Science 287:1816-1820(2000).
E. Mell, AF226382; AAR42513.1;
EMBL; AF226383; AAR42512.1;
EMBL; AF226383; AAR42512.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNV 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPVVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120
                                                                                                                                                                                                                                                                                                                      Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
-----SKDFTYSLKKELKDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 TGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTG
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                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OKT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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                                                                                                                                                                              PRT;
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Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                         Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKDANKPVRITHVVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV 539
                                                                                                                                                                                                                                                                Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                       Pizza M., Scarlato V., Manaignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin L., Moxon E.N., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.N., Grandi G., Rappuoli R.; Ildentification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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              GKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61917 MW; 4A3471514FD3C879 CRC64;
                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEBRRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2737.5; DB 2
Pred. No. 1.9e-107;
); Mismatches 29;
                                                                                                                                             592 AA
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20175756; PubMed=10710308;
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92.2%;
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                                                                                                                                           PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=860800;
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Best Local Simi
Matches 553;
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09JPS9;
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                                                                                                                                                                                                                                                                                       Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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EMBL; AF220364; AAR44213.1; --
SEQUENCE 599 AA, 62693 MW; 46C2E974AF7F78E9 CRC64;
                                 KGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFA
MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DTTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDKKKRAASVKDVLNAGWNIKGVKPGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2709; DB 2;
Pred. No. 3.1e-106;
7; Mismatches 41;
                                                                                                                                                                                                          Ā
                                                                                                                                                                                                          599
                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                         MEDLINE-20175756; PubMed=10710308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tch 88.5%;
al Similarity 89.7%;
539; Conservative 1
                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 539; Conserv
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SEQUENCE FROM N.A.
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Search completed: July 3, 2002, 08:28:47 Job time: 1168 sec

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 3, 2002, 08:31:04; Search time 104.77 Seconds (without alignments) 633.980 Million cell updates/sec Run on:

US-09-771-382-7

3044 1 MNKIYRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 598 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 segs, 111073796 residues Searched:

747574

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

1. \SIDSI\gcgdata\hold-geneseqy\geneseqp-embl/AA1980.DAT:\*
2. \SIDSI\gcgdata\hold-geneseqy\geneseqp-embl/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	A surface protein	N. meningitidis H1	A surface protein	N. meningitidis BZ	A surface protein	N. meningitidis BZ	A surface protein	BASB029 amino acid	N. meningitidis EG	A surface protein	N. meningitidis H3
		Ω		AAU06177	AAY23738	AAU06178	AAY23739	AAU06179	AAY23740	AAY57044	AAU06174	AAY23743	AAU06176
		DB	20	22	50	22	20	22	20	21	22	50	22
		Length	598	598	598	598	594	594	594	594	594	599	599
ф	Query	e Match Length DB I	100.0	100.0	99.3	99.2	97.6	97.6	93.8	93.8	93.8	92.8	92.8
		Score	3044	3044	3021	3021	2971	2971	2855	2855	2855	2824.5	2824.5
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## ALIGNMENTS

Surface protein; surface glycoprotein; infection; vaccine; A surface protein of Neisseria meningitidis. AAY23742 standard; Protein; 598 AA. (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND. 98WO-AU01031. 97GB-0026398 (first entry) immunoreactive peptide. Neisseria meningitidis. 14-DEC-1998; W09931132-A1 12-DEC-1997; 24-JUN-1999. 08-SEP-1999 AAY23742; AAY23742 RESULT 

Peak IRA; Jennings MP, Moxon ER,

WPI; 1999-418754/35. N-PSDB; AAX85794.

Neisseria meningitidis surface proteins useful for treating N. meningitidis infections

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25-JAN-2001; 2001WO-AU00069
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Best Local Similarity 100.
Matches 598; Conservative
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                          meninitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                   present sequence represents a surface protein of Neiserria
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                                                                                                                                               100.0%; Score 3044; DB 20; 100.0%; Pred. No. 1.2e-175;
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Claim 1; Page 108-110; 132pp; English
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243.598 /label= C5 /note= "Conserved region

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"Conserved region 2"

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AAMU06122-AAWU061286). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain H15 is 1 of 10 NhhA polypeptide sequences.
                                                                                                New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                Claim 9; Fig 1; 91pp; English.
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                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humans
                                The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                         Score 3021; DB 20;
Pred. No. 2.8e-174;
I; Mismatches 3;
Page 91-93; 132pp; English.
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llarity 99.3%;
Conservative
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Best Local Simi
Matches 594;
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  Claim 1;
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AMUGOISEA-ANDGIBED. The modified or mutant Nhhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain BZ10 is 1 of 10 Nhha polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
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                                                                                               /label= V1
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| Tabel = C3
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                                    Location/Qualifiers
           Neisseria meningitidis strain B210.
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/note= "Conserved
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/note= "Variable
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/note= "Variable
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N-PSDB; AAS09168.
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Length 598;

Score 3021; DB 22; Pred. No. 2.8e-174;

99.2%;

Best Local Similarity

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Query Match

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1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
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                                                                                                               PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                        SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                 glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                  A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                              AAY23739 standard; Protein; 594 AA
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N-PSDB; AAX85791.
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medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain 81.98 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh. A AUG06182-AAUG6186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
           Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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                                     Neisseria meningitidis strain BZ198
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/label= C3
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                                                                       protein of Neiserria
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      Neisseria meningitidis surface proteins useful for treating meningitidis infections
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Pred. No. 2.9e-171;
1; Mismatches 7;
                                                                          present sequence represents a surface
                                             Claim 1; Page 95-97; 132pp; English.
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WPI; 1999-418754/35. N-PSDB; AAX85792. Claim 1; Page 100-101; 132pp; English

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                 Gaps
                                        MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
                                                                                                                                                                                                                                                                                                                        YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW 598
                                                                                                                                                                                                                                                                                                                                NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
                                                                                                                             PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                           DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN
                                                                                                                                                                                                                           GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
                                                                                                                                                                                                                                                                                          DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
                                                                        SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
                 4
Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                            surface glycoprotein; infection;
Score 2971; DB 22;
Pred. No. 2.9e-171;
                                                                                                                                                                                                                                                                                                                                                                                                                             protein of Neisseria meningitidis.
               1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peak IRA;
                                                                                                                                                                                                                                                                                                                                                                              AAY23740 standard; Protein; 594
97.6%;
98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
        Similarity 98.0
6; Conservative
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QUEENSLAND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                             Surface protein;
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               Matches 586;
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Query Match
         Best Local
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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                          PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE
                                                                                                                                                                                                                                                                                                                                                                                     NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 DANKPVRITNVAPCVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                   Length 594;
                                                                                                                                                                                                   93.8%; Score 2855; DB 20; 94.6%; Pred. No. 2.9e-164;
                                                                                                                                                                                                                                 6; Mismatches
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                                                                                                                                                                                                                    Best Local Similarity 94.6
Matches 566; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY57044 standard;
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KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 480
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DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFETVTSGTKVTFASGN
                                               SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
                                                                                                                                                                                                                                                                                                                                                                                  N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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/label= C2
/tabel= C2
/ortom "Conserved region 2"
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/label- C5
/note= "Conserved region 5"
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/note= "Variable region 4"
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/note= "Variable region 2"
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/note= "Variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis strain EG327
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/note= "Conserved
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/label= C1
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                           BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
Infection; treatment; prevent; antibacterial drug.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MNKIYRIIWNSALNAWWWSELTRNHTKRASATWATAWLATLLFATWQANATDDDDLYLE
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                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide from neisseria meningitidis useful for diagnosis,
treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2855; DB 21;
Pred. No. 2.9e-164;
6; Mismatches 22;
                                                                                                                                                         /note= "Encoded by AATC"
                                                                                                                                                                                                                                                                                                                   SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 2; 74pp; English
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Best Local Similarity 94.6%;
Matches 566; Conservative
                                                                                                                                                                                                                                                        99WO-EP03255.
                                                                                                                                                                                                                                                                                     98GB-0010276
                                                                                            Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receiving the protein.
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                                                                                                                                          Misc-difference 104
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                                              BASB029:
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Jennings MP,
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                                                                                                                                                                                                                                                           The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AndU06186. The modified or mutant Nhhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences the content of the meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2855; DB 22;
Pred. No. 2.9e-164;
; Mismatches 22;
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                                                                                                                                                                                                                                       English.
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ilarity 94.6%;
Conservative (
                           25-JAN-2001; 2001WO-AU00069.
                                                     25-JAN-2000; 2000US-0177917.
                                                                               (UYQU ) UNIV QUEENSLAND.
                                                                                                          Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention.
                                                                                                                                                                                                                                     9; Fig 1; 91pp;
                                                                                                                                     WPI; 2001-488774/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                    N-PSDB; AAS09164.
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Best Local Simi
Matches 566;
02-AUG-2001
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                                                                                                            541 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW 598
                                                                                                                                      The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2e-162;
; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A surface protein of Neisseria meningitidis.
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.larity 92.7%; Pred. No. 2e-1
Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 114-115; 132pp; English
                                                                                                                                                                                                                                                                                                             AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis
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Matches 555; Conserv
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                                                                                                                                                                            480 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQ 539
DPTVHLNGIGSTLTDTLLINTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT 239
                                                                                                                                                                                                                        540 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW 598
                                   240 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKG
                                            360 NCTTATVSKDDQCNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                                                                                                                                                                                                Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                                                meningitidis H38 surface antigen NhhA polypeptide
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/label= C4
'-~to= "Conserved region 4"
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/note= "Conserved region 5"
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/note= "Conserved region
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/label= V4
/note= "Variable r
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/note= "Variable
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/label= C3
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/label= v1
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AGMO06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain 10 fil0 NhhA polypeptide sequences
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                                                                                                                                                                                                                               New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
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Best Local Similarity
Matches 555; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain H44/76. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polynuclectide sequences (AAZ39864-Z39865) and polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynuclectides and polypeptides are useful for generating an immune response in an animal. A therapeutic compositions containing BASB029 directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynuclectide is useful in the diagnosis of
                                                                                                                                                                                                                                                                                                  BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
421 gkmdetvninagnnieitrngknidiatsmtpqfssvslgagadaptlsvddkgalnvgs 480
                          New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                540 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                        BASB029 amino acid sequence from N. meningitidis strain H44/76
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                                                                                                                                                                                     AAY57045 standard; Protein; 591
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                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis.
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                                                                                                                                                                                                                                             21-FEB-2000
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the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASBO2 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial dusys. Fused recombinant protein is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NINENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG 176
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN
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                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                    DB 21; Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                               1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-
                                                                                                                                                                                                                                                                                                                                                                28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of N. meningitidis protein ORF40-1.
                                                                                                                                                                                                                                                                                                                 Score 2735.5; DB
Pred. No. 4.5e-157
9; Mismatches 28
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Best Local Similarity 91.4%;
Matches 550; Conservative
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Best Local Similarity 91.0%; Pred. No. 1.8e-156;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerse, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to used to identify immunoreactive peptides.
                    VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                     LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                                                               surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                               surface protein of Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peak IRA;
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                                                                                                                                                                                                                                                                                                                                                                                                              immunoreactive peptide
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N-PSDB; AAX85798.
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                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides proteins (AAV27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 INGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein and its nucleotide sequence, useful in vaccines or pnostic compositions for treating and/or preventing Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 20; Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                              Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.5%; Score 2725.5; DB 20; Lengt
91.0%; Pred. No. 1.8e-156;
ive 12; Mismatches 27; Indels
                                                                                                                                                                                                                                                             Rappuoli R,
                                                                                                                                                                                                                                                             Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 62; 123pp; English.
bacterial infection; treatment.
                                                                                                                                                            98GB-0022143.
98GB-0000760.
98GB-0019015.
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                                 Neisseria meningitidis
                                                                                                                                                                                                                                                              Masignani
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N-PSDB; AAX99124.
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                                                                WO9936544-A2
                                                                                                                                14-JAN-1999;
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01-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                               diagnostic
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Best Local Si
Matches 548;
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61 yldpvqrtvavlivnsdkeqtqekekveensdwavyfnekgvltareitlkagdnlkikq 120
                                         PSKGKMDETVNINAGNNI EITRNGKNIDIATSMTPOFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                                          ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                           VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                   GKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTF
                                    TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
                                                            GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                                                                                                                                                        N. meningitidis PMC21 surface antigen NhhA polypeptide sequence
                                                                                                                                                                                                                                                                                                    Surface antiqen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                                                                                                                                                                                                                               7.13bel= Mature_NhhA
/label= Mature_NhhA
/note= "Predicted mature protein, specifically
claimed in claim 12"
                                                                                                                                                                                                                                                                                                                                                                                                              /label C2
/note= "Conserved region 2"
121..124
/label= V2
/note= "Variable region 2"
125..188
                                                                                                                                                                                                                                                                                                                                                         "Conserved region 1"
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                                                                                                                                                                                                                                                                                                                                  1..51
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/label= C1
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AMAUGELAAUGGIBS). The modified or mutant Nhhh Polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen from N. meningitidis strain protein is 1 of 10 Nhh polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
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91.0%; Pred. No. 1.8e-156;
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N-PSDB; AAS09161.
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100.0%; Pred. No. 4.9e-238;
ive 0; Mismatches 0;
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US-08-409-995-2
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US-08-913-942-2
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US-09-974-32
US-09-669-974-32
US-09-668-347-44
US-08-409-995-5
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US-09-268-347-26
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US-09-268-347-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JONON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION UNBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
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1997-12-12
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Patent No. 6197312
GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: GB 97
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver: 2.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US 09-669-974-7

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Patent No. 6197312
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SOFTWARE: PatentIn Ver. 2.0
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100.0%; Pred. No. 4.9e-238;
Live 0; Mismatches 0;
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Sequence 333173

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: PEAK, Ian Richard Anselm

APPLICANT: DENNINGS, Michael Paul

APPLICANT: MOXON, E. Richard

FILE REFERENCE: 065064/0128

CURRENT APPLICATION NOWBER: US/09/669,974

CURRENT APPLICATION NUMBER: US 09/377,155

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1998-12-14

PRIOR FILING DATE: 1998-12-14

PRIOR FILING DATE: 1998-12-14

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver: 2.0
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Best Local Similarity 100.
Matches 598; Conservative
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Pred. No. 3.6e-236;
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
INNINGS, Michael Paul
TITLE OF INVENTION: E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065.064/0128
CURRENT FALING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 420
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Pred. No. 3.9e-232;
1; Mismatches 7;
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                        Sequence 7, Application US/09377155
Patent No. 6197312
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98.0%;
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Best Local Similarity 99.3%; Pred. No. 3.6e-236;
Matches 594; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                             APPLICANT: PEAK, Tan Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR PILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN OFF: 2.0
                                                                                                                                                                                                                                                                     Sequence 5, Application US/09669974 Patent No. 6333173
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US-09-669-974-5
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LENGTH: 598
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Pred. No. 3.9e-232
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                                                                                                                                                                           GENERAL INCORNATION:
APPLICANT: PEAK, IAN Richard Anselm
APPLICANT: PEAK, IAN Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
TILLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFRENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
                                                                                                                                                         Sequence 7, Application US/09669974
Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Neisseria meningitidis US-09-669-974-7
                                                                                                                                                                                                                                                                                                                                                                                                                                            97.6%;
98.0%;
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SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 98.09
Matches 586; Conservative
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US-09-669-974-7
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                                                                                                                                     Length 594;
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                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DEAK, Ian Richard Anselm
APPLICANT: DENININGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR PELLING DATE: 1998-12-14
PRIOR PILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN NOS: 33
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; Patent No. 6197312
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120 ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG 179
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 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNHIDNVDGNARAGIAQAIATAGLVQA 536
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                            1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL
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92.7%; Pred. No. 2.8e-220;
iive 14; Mismatches 29;
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: FPARK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, MICHAEL PAUL
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
                                                                                                                                     Sequence 15, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Neisseria meningitidis US-09-377-155-15
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SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity
Matches 555; Conserv
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181 PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240
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9.3e-223;
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                                                                                                                                                                                         APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, En Richard
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 9
SEQ ID NO 9
                                                                                                                     RESULT 8
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
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Best Local Similarity 94.6%;
Matches 566; Conservative
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58 YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 2.8e-212;
                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm APPLICANT: DEAK, Ian Richard Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1997-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.5%; Score 2725.5; 91.0%; Pred. No. 2.8e
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                                                 RESULT 11
US-09-377-155-21
Sequence 21, Application US/09377155
Patent No. 6197312
; GENERAL INFORMATION:
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Matches 548;
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                                                                                                                                GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: BENINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1990-08-19
PRIOR FILING DATE: 1990-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
SHOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PartentIn Ver. 2.0
SSOFTWARE: PartentIn Ver. 2.0
                                                                                                 Sequence 15, Application US/09669974 Patent No. 6333173
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Best Local Similarity 92.7%
Matches 555; Conservative
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-09-669-974-15
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61 LYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
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 530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.3%; Score 2718; DB 4; 90.7%; Pred. No. 1.1e-211;
                                                                                                                                                                                                 APPLICANT: DEAK, Tan Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: DENNINGS, Michael Paul APPLICANT: MOXON, E. Richard Paul TILE OF UNENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
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                                                                                                                                                   Sequence 2, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT ; ORGANISM: Neisseria meningitidis US-09-377-155-2
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Best Local Similarity 90.7%
Matches 547; Conservative
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                                                                                                                                                                                      GENERAL INFORMATION:
                                    QW 598
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SEQ ID NO 2
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;; Pred. No. 2.8e-212;
12; Mismatches 27;
                                                                                                                           GRUERAL INCORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michard Paul
APPLICANT: JENNINGS, Michard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFRENCE: 065064/0128
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR PAPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-13
NUMBER: OF SEQ ID NOS: 33
SEQ ID NO 21
SEQ ID NO 21
                                                                                                Sequence 21, Application US/09669974
Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 91.0%;
Matches 548; Conservative 1
               591
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590 QW
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58 YLEPVQRTAVVLSFRSDKEGTGEREGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
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 NVGSKKDNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATA
                                              -----NGINFIYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAG
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                                536 GLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVG
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                                                                                                                                                                                                  Sequence II, Application US/09377155
Sequence II, Application US/09377155
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MONZON, E. Richard
TILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 055064/0128
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Neisseria meningitidis US-09-377-155-11
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Best Local Similarity 90.59
Matches 545; Conservative
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SOFTWARE: Patentin Ver.
SEQ ID NO 11
LENGTH: 591
                                                                                             596 YQW 598
                                                                                                                     YQW 592
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US-09-377-155-11
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Best Local Similarity 90.7%; Pred. No. 1.1e-211;
Matches 547; Conservative 11; Mismatches 29;
                                                                                                                                                                                                 APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JONON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669, 974
CURRENT FILING DATE: 1099-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-104
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                     Sequence 2, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Neisseria meningitidis US-09-669-974-2
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SOFTWARE: PatentIn Ver. 2
                                                                                                                                                                                     GENERAL INFORMATION:
                                                                           590 YOW 592
                                                                                                                          RESULT 14
US-09-669-974-2
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53/ LAUAY LPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGY	530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 589
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<sup>597</sup> QW 598 || 590 QW 591 à g

Search completed: July 3, 2002, 08:37:08 Job time: 334 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

July 3, 2002, 08:33:29; Search time 58.79 Seconds (without alignments) 977.401 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-771-382-7 3044 1 MNKIYRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 598

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	adhesin NMB0992 [i	probable surface f		surface protein XF	probable autotrans	surface protein XF	probable adhesin Z		probable surface p	surface-exposed ou	hypothetical prote	AidA-I adhesin-lik	probable adhesin 2	probable adhesin h	probable adhesin P	adhesin AIDA-I pre	hypothetical prote		probable autotrans	high-molecular-wei	surface-array prot	tei	hemolysin A - Serr	hypothetical prote	puative autotransp	hypothetical prote	hypothetical prote	hesi	probable beta-barr
SUMMARIES																														
SUM	QI.	G81133	A81888	164138	D82671	AC0976	A82615	A86036	<b>Н91188</b>	AH0110	C82672	G64964	D90803	H85611	AF0394	н83135	528634	T31105	A64905	AD0123	A43855	A56143	T03415	A28182	A83080	AD0548	F90696	B98047	0	E85524
	DB			7						0	~		N	7	7	7	7	N	~	7	7	7	7	7	7	7	7	7	~	7
	Query Match Length	591	592	298	2059	1107	1190	1588	1588	658	1004	1091	949	1005	1910	1018	1286	4919	1325	3705	1536	1109	1361	1608	1417	961	5291	2551	1327	1349
đ	Query Match	ıσ	82.9	20.8	Э.	m	12.6	12.1		11.0	8.3	7.8	7.3	7.3	7.3	7.3	7.2	7.1	7.0	7.0	٠.	•	•	•	6.9		•	6.8	٠.	6.7
	Score	72	2524	633	402		382.5	368	368	335	254	236	222	222	221.5	221	220	215.5	213.5	213.5	21	211.5	210	210	209	207.5	207	206	203	203
	Result No.		7	m	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23		25	26	27	28	29

probable RTX famil	hypothetical prote		hypothetical prote	hypothetical prote	probable invasin Y	190K surface antig	hypothetical prote	hypothetical prote	probably celluloso	hemolysin [importe	adhesin/invasin, p	flagellin (importe	probable exported	probable autotrans	outer membrane pro
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6.7	9.9	9.9	9.9	6.5	6.5	6.5	6.4	6.4	6.3	6.3	6.3	6.3	6.3	6.3	6.3
203	201	200	200	199	198	197	195	194.5	193	193	192.5	192.5	192.5	192.5	191.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

GGB1131  GGB121 1  GGB122 1  GGB12
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C; Species: Haemophilus influenzae (strain Rd KW20)
C; Species: Haemophilus influenzae
C; Date: 18-Aug-1995 #text_change 24-Oct-1997
C; Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C; Accession: 164138
R; Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A; Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Accession: 164138
A; Accession: 164138
A; Accession: 164138
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82671
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-298 <TIGR>
A;Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732
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411 ISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD
                    1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 ETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 GVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471 DEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQ
                                                                                                AIATAGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAG-AITLKAGDNLKIKQNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 -INDAGTFVKVQSTEDDIEDSAATKDDN-----KNQALKAGDTLTLKAGKNLKAKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 ----DQGGKSVTFALAKDLDVKTAKVSDTLTIGGNTPAAGGATPKVSITSTADGLKLAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%; Score 633; DB 2; 47.0%; Pred. No. 3.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 KLVTGKG-KDEN-GSSTDEGE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 151; Conserv
                                                                                                                                                                                                                                          598
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A:Experimental source: serogroup A, strain 22491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                           probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S.R.; More
Rajandream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morsyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrea Mature 404, 502-506, 2000
A; Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A; Reference number: A81775; MUID: 20222556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81888
  232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESVOR-SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYI-----VVTLKAGDNL, 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                              KIKQNTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGY
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; Pred. No. 2.7e-120;
17; Mismatches 45;
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ilarity 85.5%;
Conservative 17
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A; Residues: 1-592 <PAR>
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Best Local Simi
Matches 520;
                                                                                                                                                                                                                                                                                                    QW 598
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probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C; Accession: Ac0976 C; Accession: Ac0976 C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C; Accession: Ac0976 C; Dames, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P. Nathors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A; Reference number: AB0502; PMID:11677608 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1107 <PAR>
A; Residues: 1-1107 <PAR>
A; Residues: 1-1107 <PAR>
A; Genetics: Rabbas A; Rabbas A; Rabbas B; Rabbas B; Rabbas B; A; Genetics: A;
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638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRETSATSDGVVIGYNTTDRELLGALSLGTDGESYROITNVADGSEAODAVTVROLQNAI 698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKEGTEDSNWAVYFDEKRVLKAGAITLKAGD------NLKIKQNTNE---NTNENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 TAGTNGDPTVHLNGIGSTLTDTL--LNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNI
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                                                                                                                                              2023 AVGVSAVSESGHWVFKFSGSANTRSHVGVGAGVGYOW 2059
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                                                                                                          AIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW
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B;Simpson, AJG.; Rethach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Buenno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Buenno, M.R.P.; Camargo, L.E.A.; Frrenca, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junquelra, M.L.; Remper, E.L.; Kitajima, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junquelra, M.L.; Mandelra, H.M.F.; Marino, C.L.; Marques, M.Y.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; A;Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Atelnaco, M.H.; Vallada, H.; Van Silva, F.R.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q--NTNE---NTNENTNDSSFTY---SLKKDLTDLTS---VETEKLSFGANGNKVNITSD 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KRVLKAGAITLKAGD-NLKIK 115
                         A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: 082671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNVTDDEKKRAASVKDVLNAGWNI - - - - - - - KGVKPGTTASDNVD - - - - - FVRTYDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.2%; Score 402; DB 2; Length 2059; Best Local Similarity 25.0%; Pred. No. 1.8e-12; Matches 174; Conservative 100; Mismatches 215; Indels 208;
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OY 206 TNDNVTDDEKKRAASVKDVLNAG-WNIKGVKPGTTASD	RESULT A86036 Probable e C; Species (C; Date: 11(C; Da	Query Match  Best Local Similarity 24.9%; Pred. No. 6.8e-11;  Best Local Similarity 24.9%; Pred. No. 6.8e-11;  Matches 171; Conservative 79; Mismatches 221; Indels 216; Gaps 28;  Qy 11 SALNAW-VVVSELTRNHTRRASATVATALLETATVQNATDDDLXLEPVQRTA 66
Db 814 NVAAGSADTDAVNVGOLKVTDAQVSRNTQSITNLANTQVSNLDTRYTNIENGIGDIVTTGS 873  Qy 451 PQFSSVSLGAGADAPTLSVDDE-GALNVGSKDANKPV 486  ::	A.Molecule type: DNA A.Molecule type: DNA A.Residues: 1-190 <sin- 2000="" 9a5c="" a="" a.a.;="" a.authors:="" a.c.r.;="" a.cross-references:="" a.experimental="" a.genetics:="" a.genetics<="" a.gontents:="" a.heference="" a.j.,="" a.j.s.="" a.jg.;="" a.m.;="" a.m.b.n.;="" a.p.;="" a.reference="" a.y.;="" a59128="" abreu,="" acencio,="" alvarenga,="" annotation="" arruda,="" as-neto,="" b.e.;="" briones,="" bueno,="" c.;="" c.f.m.;="" c.genetics:="" c.l.;="" c.y.;="" camargo,="" carraro,="" carrer,="" chado,="" d.m.;="" da="" de="" docena,="" e.;="" e.c.;="" e.l.;="" el-dorry,="" f.="" f.a.;="" f.c.;="" f.g.;="" f.r.;="" facincani,="" ferreira,="" gb.ae004017;="" gb:ae003849;="" genbank,="" gspdb:gn001="" h="" h.;="" h.m.f.;="" j.d.;="" j.e.;="" j.p.;="" jr.,="" june="" junqueira,="" kitajima,="" krieger,="" kuramae,="" l.e.a.;="" l.r.;="" laight="" m.;="" m.a.;="" m.c.;="" m.l.;="" m.m.;="" m.r.p.;="" m.r.s.;="" m.v.;="" madeira,="" marciuma,="" marino,="" marques,="" martins,="" menck,="" metoria,="" miracca,="" miyasi,="" nid:99107083;="" number:="" nunes,="" oliveira,="" p.;="" pidn:aaf84783.1;="" r.;="" r.g.;="" r.simpson,="" r.v.;="" reinach,="" remper,="" sa,="" santelli,="" sawasak="" silva="" silva,="" silvaina,="" source:="" strain="" submitted="" td="" to="" w.a.;=""><td>Ouery Match  12.6%; Score 382.5; DB 2; Length 1190;  Best Local Similarity 24.6%; Pred. No. 8.7e-12;  Matches 169; Conservative 89; Mismatches 226; Indels 203; Gaps 30;  Qy</td></sin->	Ouery Match  12.6%; Score 382.5; DB 2; Length 1190;  Best Local Similarity 24.6%; Pred. No. 8.7e-12;  Matches 169; Conservative 89; Mismatches 226; Indels 203; Gaps 30;  Qy

1189 FFHANSTEEDSLANGARITHNGTKGIGIGYGARVDALLAIGSRAQ-V 1245   189 FFHANSTEEDSLANGARITHNGTKGIGIGYGARVDALLAIGSRAQ-V 1245   180   181 VHLNGICSTLTDTLANGARITHNGTKGIGIGYGARVDANLAIGHAIGSRAQ-V 1245   181 VHLNGI	RESULT 9 AH0110 probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain C092) C; Species: Yersinia pestis C; Species:	Ouery Match 11.0%; Score 335; DB 2; Length 658;  216; Gaps 28; Best Local Similarity 22.3%; Pred. No. 1e-09; Matches 143; Conservative 87; Mismatches 255; Indels 156; Gaps 19;  VQRTA 66  Qy 27 TKRASATVATAVLATLLFATVQANATDDDDLXLEPVQRTAVVLSFRSDK 75
Db 1189 YEHANSTEEDSLAVGTDSLAMGAKTIVNGDKGIGIGYGAYVDANALNGIAIGSNAQ-V QY 183 VHLNGIGSTLTDTLLNTGATTNYTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP   1246   HIVNSIAIGNGSTTTRGAOTNYTAXNMDAPQNSVGEFSVGSADGOROITNVAA   QY 237 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV	HBESULT 8 H91188 H91188 C;Decies: Escherichia coli (strain O157:H7, su C;Species: Escherichia coli C;Species: H91188 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157 A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Accession: H91188 A;Accession: H91188 A;Residues: Preliminary A;Molecule type: DNA A;Residues: 1-1588 cHAY> A;Residues: 1-1588 cHAY> A;Residues: GB:BA000007; PIDN:BAB37903.1; PID:g13363955; GSPDB:GN001 A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics:	Query Match         12.1%;         Score 368;         DB 2;         Length 1588;           Best Local Similarity 24.9%;         Pred. No. 6.8e-11;         Anterior 216;         Ge           Matches 171;         Conservative 79;         Mismatches 221;         Indels 216;         Ge           QY         11 SALNAW-VVVSELTRNHTKRASATVATAULATLEATVQANATDDDLYLEPVQRTA         Indels 216;         Ge           QY         11 SALNAW-VVVSELTRNHTKRASATVATALLEATVQANATDDDLYLEPVQRTA         Indels 216;         Ge           QY         1019 SQLNATNAMIEQNTQIINQLAGNTDATYIOENGAGINYVRTNDDGLAFNDASAQGVGA         Ge         GAGINYVRTNTNDGLAFNDASAQGVGA           QY         67 VVLSFRSDKEGTEDSNWAVYFDEKRVLKAGAIT

	Qy         324 NKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTAT-VSKDDGGNITVKYDV 380           P	491 VAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQAY  1	RESULT 11  G64964 hypothetical protein b2000 - Escherichia coli C;Species: Escherichia coli C;Accession: G64964 R;Blattner, F. R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617 A;Accession: G64964 A;Status; nucleic acid sequence not shown; translation not shown	A;Wolecule type: DNA A;Wolecule type: DNA A;Residues: 1-1091 <blat> A;Residues: 1-1091 <blat> A;Gross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AAC75061.1; PID:g17883 A;Experimental source: strain K-12, substrain MG1655 C;Keywords: nucleotide binding; P-loop F;683-690/Region: nucleotide-binding motif A (P-loop)</blat></blat>
180DPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNA 227   1   1   1   1   1   1   1   1   1	11 :	C;Accession: C82672 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer Nature 406, 151-157, 2000 Nather for a complete list of authors see reference number A59328 below A;Neterion: C82672 A;Status: preliminary A;Nolecule type: DNA A;Nolecule type: DNA A;Retassidues: 1-1004 C81N> A;Cross-references: GB.ABC003881; GB.ABC003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001 A;Experimental source: strain 9a5c R;Simpson, A.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A	Dies, M. K.S.; Buendo, M. K.P.; Candargo, A.A.; Candargo, L.E.A.; Carraro, D.M.; Carrer, H. Netto, E.; Docena, June 2000  uthted to GenBank, June 2000  uthors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  i. Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr.  do, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. H. H. S.; Martins, E. M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; G.; Nunes, L.E.Y.; Oliveira, M.K.; de Oliveira, R.C.; de Santelli, R.V.; Sawasak uthors: da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, R.B.; Santelli, R.V.; Sawasak Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zofenents: annotation	· · · · · · · · · · · · · · · · · · ·

OBEST MATCH  BOBST LOGIS 141, Pred, No. 0.00019,  MACHES 145, CORRECTAINE 23.44; Pred, No. 0.00019,  MACHES 145; CORRECTAINE 23.44; Pred, No. 0.00019,  MACHES 145; CORRECTAINE 65; MARRIACHES 248; Indels 164; Gaps 25;  DB 57 LATCYRUNNHAPCANVUSELRANGERGONALSLANTSLPLANTOANATDDDDLYLE 60  110 PINE 11::!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	1 HNKIYRIIHNSALNAMVVVSELTRNHTKRASATVATAULEATVOANATDDDDLYLE 60  5 LAITZYBLUVNHITTOTLVVASELARSRCKRAGYTVATAULEATVOANATDDDDLYLE 60  5 LAITZYBLUVNHITTOTLVVASELARSRCKRAGYTVATALEATVOANATRICATOR 120  5 ST
RESULT 12 90803 AidA-1 adhesin-like protein [imported] - Escherichia coli (strain O157:H7, substrain RIV C; Species: Escherichia coli C; Species: Escherichia coli C; Species: B-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C; Accession: D90803 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gench Reference number: A99629; MUID:21156231; PMID:11258796 A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Accession: D90803 A; Status: preliminary A; Molecule type: DNA	RESULT 13 H85611 probable adhesin Z1211 [imported] - Escherichia coli (strain O157:H7, substrain EDL93 C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Species: Bscboan H85611, B8563 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May Iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Status: preliminary
A; Residues: 1-949 <hay> A; Cross references: GB:BA000007; PIDN:BAB34819.1; PID:q13360856; GSPDB:GN00154 A; Experimental source: strain 0157:H7, substrain RIMD 0509952 C; Genetics: A; Gene: ECs1396 Query Match 7.3%; Score 222; DB 2; Length 949; Best Local Similarity 22.7%; Pred. No. 0.00082; Matches 152; Conservative 89; Mismatches 263; Indels 166; Gaps 32;</hay>	A; Molecule type: DNA A; Residues: 1-1005 <sto> A; Residues: 1-1005 <sto> A; Cross-references: GB:AE005174; NID:g12514025; PIDN:AAG55356.1; GSPDB:GN00145; UWGP: A; Experimental source: strain 0157:H7, substrain EDL933 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1005 <st2> A; Residues: 1-1005 <st2> A; Cross-references: GB:AE005174; NID:g12514546; PIDN:AAG55766.1; GSPDB:GN00145; UWGP: A; Experimental source: strain 0157:H7, substrain EDL933</st2></st2></sto></sto>

34;

Length 1910;

7.3%; Score 221.5; DB 2; 22.2%; Pred. No. 0.0022; 85; Mismatches 259;

Indels

us-09-771-382-7.std.rpr

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A;Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175
C;Genetics:
A;Gene: hmwA
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1251 GIDFYGANTLNIIKGSQLSLLGENKGAQDTAGGNGISYTSLAKLTVNNNGSLKMEGRSTS 1310
                                                                                                                                                                                                                                                                                                                                --ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1311 GTGINFPSSNNTLVFNGDGDTLIKGSSVAGTGAAISGVVNNSTGPWTIEGISTDGAGVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 V--KPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIG--AKTSVIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 -----ETVNINAGN----NIEITRNGKNIDIA-TSMTPOFSSVSLGA--GADAPTLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 IAQAIATAGLAQAY-LPGKSMMAIGGGTYRGEAGYAIGYSS-ISDTGNWVIKGTASGNSR
                                                                                                                                                                                                     TA---VVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGA-ITLKAGDNLKIKQNTN-
                                                                                                                                                                                                                                                                              178 NGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDV----LNAGWNIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               470 DDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAG--
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Matches 160; Conservative
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0394
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutharford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SMMAIGGGTYRGEAGYA---IGYSS--ISDTGNWVIKGTASG 582
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                                                                                                                                                                                                                                                                           ----KVVQAGETVNDGT----LINHDNQIVFG-----TANGMTISTG--LELGPDSEE 153
                                                                                                                                                                                                                                                                                                                    NTN----EN----TNDSSFTYSLKKDLTDLTSVETEKLSFGA---NGNKVNITSDTKGLN 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
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                                                                                                                                                                MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 166;
                                                                                     Length 1005;
                                                                                     Query Match 7.3%; Score 222; DB 2; La
Best Local Similarity 22.7%; Pred. No. 0.00089;
Matches 152; Conservative 89; Mismatches 263;
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A; Molecule type: DNA
A; Residues: 1-1910 <KUR>
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                             A; Gene: Z1211; Z1651
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               C; Genetics
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1370

-----SSGKVISGNVSPSKGKMD-

377

--- IDAVNKAGWR

1430

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probable adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PA01)
C; Species: Pseudomonas aeruginosa
C; Species: 15-5ep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C; Accession: H83135
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yann, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1018 <STO>
A; Cross-references: GB: AE004824; GB: AE004091; NID: g9950277; PIDN: AAG07469.1; GSPDB: GN001
A; Experimental source: strain PAO1
C; Genetics:
A; Gene: PA4082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VDFVRTYDTVEFLSADTKT 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304 ------GKVMVGGALSANALNGPG------HGGTVEVRGQAVE---VALGTQVNTL 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 PTLSVDDEGALNVGSK------DANKPVRI------TNVAPGVKEGD 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 VTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQAYLPGKSMMAIGG--GTYRG 557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 GNVSPSKG--KMDETVNINAGNNI-----EITRNGKNIDIATSMTPQFSSVSLGAGADA 464
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                                                                                                                                                                                                                     7.3%; Score 221; DB 2; Length 1018;
22.1%; Pred. No. 0.001;
Live 89; Mismatches 209; Indels 230;
A; Reference number: A82950; MUID: 20437337
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537 TLDGLGNSIGNLSISNTG 554
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Best Local Similarity 22.15
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Search completed: July 3, 2002, 08:38:17 Job time: 288 sec THIS PAGE BLANK (USPTO)

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

July 3, 2002, 08:37:14; Search time 29.79 Seconds (without alignments) 777.250 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-771-382-7 3044 1 MNKIYRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 598

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	es	Q03155 escherichia	P32051 escherichia	P15320 serratia ma	P15921 rickettsia	P16466 proteus mir		Q52657 rickettsia	Q9kka3 r outer mem			_	_		P52143 escherichia	P25927 salmonella	006653 r outer mem			Q08860 shigella fl		P37710 enterococcu		_	Q48253 helicobacte	P45355 haemophilus	_	Q09624 caenorhabdi	P45354 haemophilus	9	ď	60	Q06982 salmonella
SUMMARIES	. QI	AG43_ECOLI	AIDA_ECOLI	YDEK_ECOLI	HLYA_SERMA	OMPA_RICRI	HLYA_PROMI	OMPB_RICRI	OMPA_RICCN	OMPB_RICCN	120K_RICRI	ICEN_XANCT	YDBA_ECOLI	WAPA_BACSU	YMJB_CAEEL	YPJA_ECOLI	BIGA_SALTY	OMPB_RICJA	OMPB_RICTY	SLAP_CAMFE	FLIC_SHIFL	APU_THETU	ALYS_ENTFA	OMPB_RICPR	SLAP_BACST	VAC3_HELPY	HXA3_HAEIN	SLAP_CAUCR	YS89_CAEEL	HXA2_HAEIN	FLIC_SALCH	PMPB_CHLMU	FLIC_SALNA	FLIC_SALRO
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ď	Query Match	7.8	7.2									•	٠		•	ر 9			•	'n.	S		ഗ	S	S	S	2	S	S	2	S	ņ	5.3	5.3
	Score	236	220	213.5	210	197	190	188	187	184.5	183.5	183	182.5	182.5	181.5	180	180	178.5		174.5	171	169.5	168	168	167		165.5		w	163.5	163	163	162	162
	Result No.	1	7	3	4	S	9	7	<b>&amp;</b>	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33

Q9pjt6 chlamydia m P04949 escherichia	Q06983 salmonella P45387 haemophilus	Q06971 salmonella	P19570 bacillus sp	P45384 haemophilus		P56867 deinococcus	P06620 pseudomonas	P45508 escherichia	P80544 staphylococ
Y741_CHLMU FLIC_ECOLI	FLIC_SALSE HAP_HAEIN	FLIC_SALDU	GUN3_BACS4	IGA2_HAEIN	PMPC_CHLTR	HPI1_DEIRA	ICEN_PSESY	YFAL_ECOLI	MRSP_STAAU
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1007	504 1394	504	825	1702	1770	948	1200	1250	1637
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162 161	161 161	160	160	160	160	159.5	159.5	159	159
34	36 37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 IGYSSISDIGNWVIKGTASG 582
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Q03155;
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AIDA_ECOLI
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                                                                                                                           FEMS Microbiol. Lett. 149:115-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.8%; Score 236; DB 1; Length 1039;
13.4%; Pred. No. 0.00012;
ve 63; Mismatches 248; Indels 164; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P3-----TUANHDNQ 74
                                                                                  "Antigen 43, a phase-variable bipartite outer membrane protein, determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                     SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
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STRAIN ML 308-225).
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SL -> FF (IN STRAIN ML 308-225).

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V -> F (IN STRAIN ML 308-225).

V -> F (IN STRAIN ML 308-225).

A TN -> STI (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

N -> O (IN STRAIN ML 308-225).

E -> V (IN STRAIN ML 308-225).

H -> Y (IN STRAIN ML 308-225).

H -> Y (IN STRAIN ML 308-225).

H -> Y (IN STRAIN ML 308-225).

C -> K (IN STRAIN ML 308-225).

H -> Y (IN STRAIN ML 308-225).

C -> K (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).

LULVHTS -> MULIYNA (IN STRAIN ML 308-225).

LONY -> LGA (IN STRAIN ML 308-225).

QGT -> LGA (IN STRAIN ML 308-225).

QGT -> LGA (IN STRAIN ML 308-225).

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                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.
-i- SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTIGEN 43 ALPHA CHAIN.
ANTIGEN 43 BETA CHAIN.
K -> N (IN STRAIN ML 306
SL -> FF (IN STRAIN ML 3
                                                                    Henderson I.R., Meehan M., Owen P.,
"Antigen 43, a phase-variable bipartite outer
                                                                                                                                                                                                                                                                                                                                                                                                                    Ecodene, EG12686; flu.
Outer membrane, Signal; Complete proteome.
SIGNAL 1 52
in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000291; AAC75061.1; ALT_INIT.
EMBL; D90838; BAAL5825.1; ALT_INIT.
EMBL; D90839; BAA15832.1; ALT_INIT.
EMBL; U24429; AAB47869.1; -.
                                                        MEDLINE=97257509; PubMed=9103983;
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Best Local Similarity
Matches 145; Conserv
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121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180
                                                                                                                                         PTVHLNGIGSTL----TDTLLNTG-----ATTNVTNDNVTDDEKKRAASVKDVLNA 227
                                                                                                                                                                                                                                                                                                                                                     GWQV -- VKPGTVATDTV -- VNTGAEGGPDAENGDTGQFVRGDAVRTTIN----KNGRQIV 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 GVAGNT-----TVNQKGRLQVDAGGTAT-----NVTLK------
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
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STRAIN=2787 (0126:H27);
MEDLINE=92326538; PubMed=1625582;
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                                                                                                                                                                                                                                           TVSSG------ETQIVYSGRGNSNATVNSGGTQIVNNGGKTTATTVNSSGSQNVGTSGA 113
                                                                                                                                                                                                                                                                   -----DSNWAVYFDEKRVLKAGAIT--- 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 HIRNGGIASGTIVNQSGY------VNISSGGYAESTIINSGGTLRVLSDGYA 395
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                                                                                                                                                                                                                                                                                                                     106 -LKAGDNLKIKQ-NTNENTNESFTYSLKKDL-TDLTSVETEKLSFGANGNKVNIT
                                                                                                                                                                                                                                                                                                                                   ----TG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 NSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRGIWYSNFLTAVWSMFPGTASGANVNLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | | : ::: | | : | | : | | GATLPELTTMAALSVSQNHASNIVLENGGLLRVTSGGTATDTTVNSAGRLRIDDGGTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTINADGIVAGINIQNDGNFILNLAENYDFETELSGSGVLVKDNTGIMTYAGTLTQAQG
                                                                                                                                                                                                                                                                                                                                                                                                                      TGATTNVTNDNVTDDEKKRAASVKDVLNAG----WNIKG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 -VKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKE--K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGKLVTGKGKD--ENGS------STDEGEGLVTAKEVIDAVNKAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSGWNLDSKAVAGSSGKVI--SGNVSPSKGKMDETVNINAGN---NIEITRNGKNIDIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 -----VGSKDANKPVRITNVAP-----------
                                                                                                             Ouery Match 7.2%; Score 220; DB 1; Length 1286; Best Local Similarity 17.4%; Pred. No. 0.00091; Matches 160; Conservative 106; Mismatches 290; Indels 362;
                                                                                                                                                                                                                  52 TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEGTE-------------
                                                                           SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
EMBL; X65022; CAA46156.1; -.
PIR; S28634; S28634.
Ccall adhesion; Signal; Outer membrane; Plasmid.
SIGNA
                                                    ADHESIN AIDA-I.
                                                                                                                                                                                                                                                                                                                                                                     SDTKGLNFAKETAGTNGDPTVHLNG-----
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                                                               1286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makin T., Mizobuchi K., Mori H., Mori T., Motomura K., Makada S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wamamoto Y., Horiuchi T., Takeuchi Y., Wanamoto Y., Horiuchi T., Takeuchi Y., Wanamoto T., Takeuchi T., Saito N., A 570-kb DNA sequence of the Escherichia coli K.12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94100243; PubMed-8274505; Cartwright P.J., Tinms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.; "An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and MOM38.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
STRAIN=KIZ / MG1657,
STRAIN=KIZ / MG1657,
PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maynew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Gray Shao Y.;
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-!- SIMILARITY: TO E.COLI YFAL.
-!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                            P32051; P76140; P77168; 01-0CT-1993 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 140-CCT-2001 (Rel. 40, Last annotation update) Hypothetical lipoprotein ydeK precursor (ORFT).
1325 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S34315, S34315.
EcoGene; EG11780; ydeK.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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EMBL; D90794; BAA15197.1; ALT_INIT.
EMBL; X73295; CAA51730.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97251357; PubMed=9097039;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 595-1325 FROM N.A.
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    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562;
    YDEK_ECOLI
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SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
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                                                                                                                                                                                             61 PVQRTAVVLSFRSDKEGTG---EKEGTEDSNWAVYFDEKRV--LKAGAITLKAGDNLKIK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIA---TAGLAQAYLPG 544
                                                                                                                                Gaps
                                                                                                                                                                                                           NSVITNEGTNEGYDGHGEMNISNQGLVVSNGGSSLGYGETGVGNVSITTGGMWEVNKNVY
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                                                                                                                                                   1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
                                                                                                                                                                                                                                       116 QNT-----NENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNI-TSDTKGL
                                                                                                                                                                                                                                                                                 N------FAKETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRA
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                                                                                                                                                                                                                                                                                                                                                                                           229 KGG--EWLIKNNDSSIEFQIGNQGTGEATIREGGLVTAENTIIGGNATG----IGTLNVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DQDSVITVRRLYNGYFGNG---TVNISNNGLINNKEYSLVGVQDGSHGVVNVTDKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNV-----GSKDANKPVR
                                                                                                                                                                                                                                                           105 TITTSVIGANEDSEGTVNVLGGTWRL------YDSGNNARPLNVGQSGTGTL
                                                                                                                                                                                                                                                                                                                                                                                                                 339 TGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVK-YD-VNVGDALN--VNQLQNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                               Indels 159;
                                                                                                          Length 1325;
                   POTENTIAL.
HYPOTHETICAL LIPOPROTEIN YDEK.
N-ACYL DIGLYCERIDE (POTENTIAL).
N -> K (IN REF. 3).
M -> S (IN REF. 3).
My; 26A3A066FA19AD7D CRC64;
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                                                                                                                                                                  Hypothetical protein; Membrane; Lipoprotein; Signal;
                                                                                                        7.0%; Score 213.5; DB 1;
ilarity 22.7%; Pred. No. 0.002;
Conservative 72; Mismatches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
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1325 AA; 136514 N
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                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 GWNL-----
                                                                                                                              Matches 147;
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                                                   CONFLICT
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Best Local
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                                                                        SEQUENCE
                    SIGNAL
                               CHAIN
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                                                                 hemolysin determinant of Serratia
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                                                                                                                                                                                                                                                                 FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
                                                                                                      marcescens.";
J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396 REQLQQAGSTVAASGSAKLISTQEDVKLLGANVSADRALSVKAARDVHLAGLVEKDKSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 RGYQRNHTSSLRTGRWS-NSDESESLKASELRSEGELTLKAGRNVS-TQGAKVHAQRDLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 IDADNQIQVGVQK-TANAKAVRDDKTSWGGIGGGDNKNN--SNRREISHASEL--TSGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 TVHLNG-IGSTLTDTLL--NTGATTNVTNDNVTDDEKKRAASVKDVLNA----GWNIKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 KDGKLVTGKGKDENGSSTDEGEGLVT----AKEVIDAVNKAGWRM-----KTT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----TANGQTGQADKFETVTSGTKVTFASGNGTTA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89; Mismatches 275; Indels 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.9%; Score 210; DB 1; 22.1%; Pred. No. 0.0036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hemolysis; Toxin; Outer membrane; Signal.
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MEDLINE=88257037; PubMed=3290200;
Poole K., Schiebel E., Braun V.;
"Molecular characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M22618; AAA50323.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 22.19
Matches 159; Conservative
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                         955 KGEVRDQGTQYQASKG-AVNLTADSHRSEAAANRQDEQSRDTRGSAGVRVYTTTGSDLTV 1013
                                                                                                                                                                                1014 DAKG----EGGTQRSNSSASQAVTGSIDAANGINVNVKKDAIYQGTALNGGRGKTAVNA 1068
                                                                -----TNVAQLKGVAQNLN------NILDNVDGNARAGIAQAIATAGLAQAYL 542
:| | | | | :: | | | | :: | 896 AVGKAAKLDA-TGVINDIGGIGAPNVGLDIGAGGSSEKRSSSSQAVVSSVQAGSIDINA 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
"A protective protein antigen of Rickettsia rickettsii has tandemly
repeated, near-identical sequences.";
Infect. Immun. 58:2760-2769(1990).
-!- FUNCTION: ELLCITTS PROTECTIVE IMMUNITY.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                  01-APR-1990 (Rel. 14, Created)
1-APR-1990 (Rel. 14, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa antigen) (Cell surface
                                                                                                                                                    543 PGKSMMAIGGGTYRGEAGYAIGYSSISDTGNW-----VIKGTASGNSRGHFGASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OUTER MEMBRANE PROTEIN A.
13 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTW: GLYCOSYLATED (PROBABLE).
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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B (TYPE II).
C (TYPE II).
D (TYPE II).
E (TYPE II).
F (TYPE II).
G (TYPE II).
I (TYPE I).
J (TYPE I).
J (TYPE II).
K (TYPE II).
K (TYPE II).
M (TYPE 
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                                                                                                                                                                                                                                                                                                           2249 AA
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Antigen; Repeat; Signal; Cell wall;
SIGNAL
                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen) (rOmpA) (rOmp A)
                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rickettsia rickettsii.
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P15921;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 IKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFTGNSTVTGNVGNTNALATVN 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 AVKFIN--PVVVTGAIDNTG------586
                                                                                                                                                                                                                   --GAI-----TLKAGDNLKIKQ 116
                                                                                                                                                                                                                                                                          87 GGDYTVTADAADRIIKAINVAGTTPVGLNITQNTVVGSIITKGNLLPVTLNAGKSLFLNG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197 GGIITVKTDAAINGT-----IGNTNALATVNVGAGTATLGGAVIKATTTKLTNAASVL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 KAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNIT---VKYDVN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 VGAGLLQ----VQGGVVKANTINLTDNASAVTFT--NPVVVTGAIDNTGNANNGIVTFTGN 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 STVTGDIGNTNALATVNVGAGTATLGGAVIKATTTKLTNAASVLTLT-NANAVLTGAIDN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437 TRNGKNIDIAT-----SMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIANE 9017082; PubMed-2407716; Uphoff T.S., Welch R.A.; Uphoff T.S., Welch R.A.; Noclectide sequencing of the Proteus mirabilis calcium-independent "Nuclectide sequencing of the Proteus sequence similarity with the Serratia marcescens hemolysin genes (shla and shlB)."; J. Barteriol. 172:1206-1216(1990).

-1. FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                         Gaps
                                                                                                         34 VATAVLATLLFATVQANATDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYF 93
                                                                                                                                            39 VATGVIATNNNAAFSNNVGNNN---WNEITAAGV-----ANGTPAGGPQNNWAFTY
                                                                                                                                                                                                                                                                                                                             NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANG------NKVNITS--DT
                                                                                                                                                                                                                                                                                                                                                                                                                                             166 KGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNV----TDDEKKRAASVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 DYLNAGWNIKGYKPGTTASDNVDFVRTYDTVEFLSADTKTT----TVNVESKD---NG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 -KKTEVKIGAKTSVIKEKDGKLVTG----KGKDENGSSTDEGEGLVTAK----EVIDAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---VGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINA--GNNIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVRITUVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARA----GIAQAIATAGLAQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        484 TTGGDNVGVLNLNGALSQVTGNIGNTNSLATISVGAG--TATLGGAVIKATTTKLTDAAS
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6.5%; Score 197; DB 1; Length 2249; 2.3%; Pred. No. 0.023;
                                                   Indels
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                                                      261;
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01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1577 AA
                                                   71; Mismatches
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                            22.3%;
                                                      Matches 143; Conservative
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                                                                                                                                                                                                                      94 D-----EKRVLKA-
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                            Similarity
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                                  Local
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1334
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                                                                                               OMPB_RICRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 159;
                                                                                                                                                                                                                                                                                                                       STRAIN=R;
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                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEKVGT--TPE--SKDYGGGFNAGTTHHSKEQTTAKVGTITGSQGIELNAGHNLTLQG-- 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         987 TLDKHQTTFHETKGGGQIGVSTKTGSDITVAIKGEGQTT------DNALMETKAKGSQF 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1040 TSNGDISINVGENAHYEGAQFDAQKGK---TV-INAGGDLTLAQATDTHSESQSNVNGSA 1095
                                                    SUBCELLULAR LOCATION: Outer membrane.

SUBCELLULAR LOCATION: Outer membrane.

MAI SERLAMBOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.

SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      441
                                                                                                                                                                                                                                                                                                                                                                                                                                619 TNKQTSTGSELISDAQLTVVSGNDVNVIGSLIKSADKLGIHSLGDINVKSAQQVTKIDDE 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KPG---TTASDNVDF---VRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --DKFETVTSGTK----VTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGW 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNINENTNENTNDSSF 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----HITHTHNKNTSTETEOANS 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 TYS-----LKKDLT----DL-----TSVETEKLSFGANGNKVNITSDTKGLNFAKET 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --DNTDTTISGGFSYTGGVDKVGSKADFQYDKQHTQTEVTKNRGSQTEVAGDLTITANKD 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLHEGASHHVEGRYQESGENIQHLAVNDSETSKTDSLNVGIDVGVNLDYSGVTKPVKKAI 884
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      ------VLATLLFATVQANATDDDDLYLEPVQRTAVVLSF 71
                              THE ERYTHROCYTE MEMBRANE. HPMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --NLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITR------NGK-
               FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       720 TISGANVDLQANKDVTFAGSDLKTTAGNASITGDNVAFVSTENK------KQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 AGTNGDPTVH-----LNGIGS------TLTDTLLNTGATTNVTND-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDGVNTTKPGNNTDLTKKVTARDAIANLA----NLSNLETPNVGVEVGIKGGG--SQQS
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                                                                                                                                                                                                                                                                                                                                                                           238;
              HEME - IRON
                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 190; DB 1; Length 1577;
                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----NVTDDEKKRAASVKDVLNAGWNI----
                                                                                                                                                                                                                                                                                                       1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;
              RELEASES
                                                                                                                                                                                                                                                                                                                                                            ilarity 20.1%; Pred. No. 0.034;
Conservative 101; Mismatches 227;
              WHICH
                                                                                                                                                                                                                                                                 Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                            HEMOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   679 KTSLAITGHAKEVEDKQYSAGF-----
                         ERYTHROCYTES BY INTERACTION WITH
              CELL-BOUND HEMOLYSIN,
                                                                                                                                                                                                                                    EMBL; M30186; AAA25657.1; -.
                                         REQUIRES HPMB FUNCTION.
                                                                                                                                                                                                                                                                                         1577
                                                                                                                                                                                                                                                                                                                                                                                                    TRNHTKRASATVATA
                                                                                                                                                                                                                                                    PIR; A35140; A35140
                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                              SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                     Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB) (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-90136087; PubMed=2515418;
Gilmore R.D. Jr., Joste N., McDonald G.A.;
Mol. Surface-exposed protein of Rickettsia rickettsii.";
Mol. Microbiol. 3:1579-1586(1989).
I- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMINOGEN DURING INFECTION.
I-SUBCELLIGHAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A LAYER WITH HEXAGONAL. SYMMETRY.
I-SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor."; Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 KDA SURFACE-EXPOSED PROTEIN. 32 KDA BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.2%; Score 188; DB 1; Length 1654; 31.9%; Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                              ---INNSGNLTINGNS 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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543 PGKSMMAIG------GGTYRGEAGYAIGYSSISDTGNWVIKGTA
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                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                               1654 AA
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|1205 -GSAQFAIGKQDEKSVSREGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia rickettsii
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1654 AA;
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MEDLINE=21442074; PubMed=11557893;
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  RRARAR RR
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MEDLINE=94171067; PubMed=8125327;
Crocquet-Valdes P.A., Weiss K., Walker D.H.;
"Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
Gene 140:115-119(1994).
                                       ---NENTNENTND----SSFTYSLKKDLTDLTSVETEKLSFGANG 156
                                                                             341
                                                                                                                                                                                                                                                                                307
                                                                                                                                                                                                                                                                                                                                                                                                       568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       430 AGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEG----ALNVGSKDANKP 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                684 NGTTLAA---GTNLGSATNPLAEINFGSKGVNVDT-VLNV-GEGVNLYATNITTTDANVG 738
241 GIIFNTDANNANTLNLQAGGT-TINFTGTDGTGRLVLLSKHAAATNFNITGSLGGNLKGV 299
                                                                                                                                                        342 KVATIDGQVYAKDMVIQSANATGQVNFRHIVDVGADGTTAFKTAASKVTITQDSNFGNTD 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           739 SFVFNAGGTNIVSGTVGGQQGNKFNTVALENGTTVKFLGNATFNGNTTAANSTLQIGGN 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Outer membrane protein A precursor (190 KDa antigen) (Cell surface
                                                                                                                                                                                                                                                                                                         ----VESKDNG-----GKTEVKIGAKTSVIKEXDGKLVTGK------GKDENGSST
                                                                                                                                                                                                                                                                                                                                                                                                     517 LDGSATITGD--IGNAGGAAALQRITLAN-----DAKKTLTLGGANIIGAGGGTIDLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     486 VRI-----TNVAPGV---KEGDVTNVAQLKG--VAQNLNNRIDN------VDGN
                                                                                                                  157 NKVNITSDTKGLNFAKETAGTNGDPTV-HLNGIGSTLTDTLLNTGATTNVTNDN--VTDD
                                                                                                                                                                                               214 EKKRAASVK--DVLNAGWNIKG--VKPGTTASDNVDFVRTYD---TVEFLSADTKTTTVN
                                                                                                                                                                                                                                       402 FGNLAAQIKVPNAITLIGNFTGDASNPGNTAG-----VITFDANGTLESASADANVAVTN
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Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;
Q52670; Q52674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                          300 IEFNTVAVDGQLTANAGAANAVIGTNNGAGRAAGFVVSVD----
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SEQUENCE FROM N.A.
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                                       114 IKQNT----
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                    STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;
MEDLINE=97015921; PubMed=8862558;
Roux V., Fournier P.E., Raoult D.;
"Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rOmpA.";
J. Clin. Microbiol. 34:2058-2065(1996).
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R -> H (IN STRAIN INDIAN TICK TYPHUS).

MISSING (IN STRAIN MI).

MISSING (IN STRAIN MOROCCAN).

Y -> II (IN STRAIN INDIAN TICK TYPHUS)

D -> A (IN STRAINS INDIAN TICK TYPHUS).
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M -> I (IN STRAIN INDIAN TICK TYPHUS).

Q -> K (IN REF. 1).

I -> V (IN REF. 1).

I -> I (IN REF. 1).

T -> I (IN REF. 1).

G -> D (IN REF. 1).
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KATLGGAIIKATTTK -> LLQVQGGVVKANTIN (IN
                                                                                 "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
   Fournier P.-E., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Indian tick typhus, MI, Malish 7, and Moroccan;
Raoult D., Fournier P.E., Roux V.;
"Phylogenetic analysis of spotted fever group rickettsiae by study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the outer surface protein rOmpA.";
Submitted (DEC-1996), to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ELICITES PROMECTIVE IMMUNITY (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED IS S-LAYER WHITH HEXACONAL. SYMMETRY.
-!- PTM: GLYCOSYLATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OUTER MEMBRANE PROTEIN A. THR-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch)
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U43794; AAB49549.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U01028; AAA17405.1; -.
                                                                                                                                                                              SEQUENCE OF 8-204 FROM N.A.
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-----GYSSISDTGNWVIKGTASGNSR 585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 GDNLKIKQNTN-----ENT-NEN-----TNDSSFTYSL-KKDLTDLTSVETEKLSF 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTLLNTGA------TTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240
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"The rickettslal outer membrane protein A and B genes of Rickettsla australis, the most divergent rickettsla of the spotted fever group.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: THE 120 KDA SURFACE EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
SALVLSNLTGVGVNNILLAADLVAPGVDEGTVVFDGGVNGLNIGSNVA---GAARN---- 1107
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2005 (Rel. 41, Last annotation update)
01-MAR-2007 (Rel
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FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Phylogenetic analysis of members of the genus Rickettsia using the
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SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                      IDNVDGNA-----RAGIAQAIATAGLAQAYLPGK----SMMAIGGGTYR-GEAGYAI
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Rickettsiaceae; Rickettsieae; Rickettsia.
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Int. J. Syst. Evol. Microbiol, 50:1449-1455(2000).
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RESULT 10
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                                                                        32 KDA BETA PEPTIDE.

9 -> A (IN STRAIN INDIAN TICK TYPHUS).

6 -> S (IN STRAIN INDIAN TICK TYPHUS).

8 -> N (IN STRAIN INDIAN TICK TYPHUS).

9 -> A (IN STRAIN INDIAN TICK TYPHUS).

10 -> V (IN STRAIN INDIAN TICK TYPHUS).

11 -> V (IN STRAIN INDIAN TICK TYPHUS).

12 A -> T (IN STRAIN INDIAN TICK TYPHUS).

13 A -> T (IN STRAIN INDIAN TICK TYPHUS).

14 -> L (IN STRAIN INDIAN TICK TYPHUS).

15 -> C (IN REF. 3).

16 -> C (IN REF. 3).

17 C (IN REF. 3).

18 -> C (IN REF. 3).

19 C -> C (IN REF. 3).

10 C -> C (IN REF. 3).

11 C -> C (IN REF. 3).

12 C -> C (IN REF. 3).

13 C -> C (IN REF. 3).

14 -> R (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                         Indels 149;
                                                                                                                                                                                                                                                                                                                                                         Length 1655;
      EMBLA ALTERIOR SESS. TOMPA_TOMPB.

Pfam: PF02708; TOMPA_TOMPB: 1.

Antigen; S-layer; Cell wall; Complete proteome.

CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                      6.1%; Score 184.5; DB 1;
22.1%; Pred. No. 0.067;
Live 76; Mismatches 292;
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AAD39533.1;
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                                                                                                                                                                               Gilmore R.D. Jr., Joste N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encoding the 120 kb surface-exposed protein of Rickettsia rickettsii.";
Mol. Microbiol. 3:1579-1586(1989).
-!- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNGEN DURING INFECTION.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
-!- MISCELLANBOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES
                                                                                                                                                                                                                                                                                           CONFERRING ANTIGENICITY TO THE PROTEIN.
                                                                                               Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                     01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1300 AA
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IS $07575, $07575.
InterPro; IPR003858; rOmpA_rompB.
Pfam; PF02708; rOmpA_rOmpB; 1.
Pfam; PF02708; rompA_rompB; 1.
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                                                                                                                                                          STRAIN=R;
MEDLINE=90136087; PubMed=2515418;
                                                           120 kDa surface-exposed protein
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X16353; CAA34402.1; -.
                                                                                     Rickettsia rickettsii
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       655
698
                                                                                                                       NCBI_TaxID=783;
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us-09-771-382-7.std.rsp

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Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                     gene inaX
                                                                                     nucleation
                                                                                   "Conserved repetition in the ice nucleat
Xanthomonas campestris pv. translucens."
Mol. Gen. Genet. 223:163-166(1990).
                                                               MEDLINE=91080859; PubMed=2259339;
                                                                                                                                                                                                                                                                                                                         EMBL; X52970; CAA37140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                           Zhao J., Orser C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 115; Conserv
                                           FROM N.A.
                                                                                                                                                                                                                   FAMILY
                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                     37;
                                                                                                                                                                                                                                                                                                                                                                                DSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN--ENTNENTNDSSFTYSLKKDLTDLT 143
                                                                                                                                                                                                                SI--FKLADGTVING-KVNQTA-----LVGGALAAGTITLDG-SATITGDIGNAGG 178
                                                                                                                       : || :| | |:|:
LVIGNDGAVQFAHDTYLITRTINAAGQGKIIFNPVVNNGTTLAAGTNLGSATNPLAEINF
                                                                                                                                                                                                                                                                                                                                                                                                                            30 ASATVATAVLATLLFATVQAN--ATDDDDLYLEPVQRTAVVL--SFRSDKEGTGEKEGTE
                                                                                                                                                                      ----VITFDANGTLESAS----ADANVAVINNITAIEASGAGVVQLSGTHAAELRLGNAG
                                                                                                                                                                                            SVETEKLSFGA - - NGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNTGA
                                                                                                                                                                                                                                                            179 AAALQRITLANDAK-----KTLTLGGANIIGAGGGTIDLQANGGTIKLTSTQNNIVVDF
                                                                                                                                                                                                                                                                                 ---VRTYDT-----VEFLSADTKTTTVNVESKDNGK-----KT----E
                                                                                                                                                                                                                                                                                                                                                                                                              --SGTKVTF---ASGNGTTATVSKDD---QGNITVKYDVNVGDALNVNQLQNSG---WNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAGNNIEIT-----RNGKNIDIATSMT-------PQFSSVSLGAGAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGNIIATNATINDGVTVTTGGIAGIGFDGK - - ITLGSVNGNGNVRFADGILSNSTS - - - M
                                                                                                                                                                                                                                        -TASDN - - - VDF
                                                                                                                                                                                                                                                                                                                                                                    --EGEGLVTAKEVIDAVNKAGWRMKTTTAN--------GQTG--QADKFETVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --APTLSV-----DDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIDNVDGNARAGIAQAIATAGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWV
                                                                                                                                                                                                                                                                                                                            VKIGAKTSVIKEKDGKLVT-----GKGK-------DENGSSTD----
                                                                Length 1300;
N-LINKED (POTENTIAL).
N-LINKED (POTENTIAL).
N-LINKED (POTENTIAL).
M. E09E52C3F647243D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSKA-----VAGSSGKVIS--GNVSPSKGKMDETVNI-----
                                                                                    93; Mismatches 273;
                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
                                                                         Pred. No. 0.056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1567 AA.
                                                                                                                                                                                                                                       TINVINDNVIDDEKKRAASVKDVLNAGWNIKGVKPGT
                                                                6.0%; Score 183.5; 21.8%; Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. translucens).
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                                 132801
                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ice nucleation protein.
 \frac{1140}{1246}
1140 11
1146 11
1211 12
1300 AA;
                                                                          Similarity
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01-NOV-1990
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                                                                                     Matches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ICEN_XANCT
P18127;
           CARBOHYD
                      CARBOHYD
                                 SEQUENCE
                                                                Query Match
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CRYSTALIZATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CRYSTALIZATION IN SUPERCOOLED WATER.
-!- SUBCELDULAR LOCATION: OUTER membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSIS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PRIODICITY IS SUPERIMPOSED.
-!- MISCELLANBOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICH
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
-!- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        735 GSTQTSGSDSSLTAGYGSTQTARKGSDVTAGYGSTGTAGADSTLIAGYGSTQTSGSDSSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   906 ---VTAGYGSTG----TAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTARKGSDMTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN-----ENTNENTNDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYSLKKDLT----DLTSVETEKLSFGA------NGNKVNITSDTKGLNFAKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282 AKTSVIKEKDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 AVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGYGSTQTARKGSDITAGYGSTGTAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.0%; Score 183; DB 1; Length 1567; 20.2%; Pred. No. 0.074; Live 83; Mismatches 274; Indels 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIRS. $11672; $11672.

HSSP: P06620; ILNA.

InterPro: IPR000258; Ice_nucleatn.

Pfam: PF00818; Ice_nucleation; 81.

PRINTS; PR00327; ICENUCLEATN.

PROSTTE; PS00314; ICE_NUCLEATION; 57.

Ice nucleation; Repeat; Outer membrane.

SEQUENCE 1567 AA; 152548 WW; C8B451D959ECAD63 CRC64;
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19;

I -> V (IN REF. 2). I -> V (IN REF. 2). My; B83A12C8B53220EE CRC64;

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EMBL, X62680; -; NOT_ANNOTATED_CDS.
EcoGene; EG11307; ydba.
Hypothetical protein; Complete proteome.
D90778; BAA18880.1; ALT_SEQ
                                                                                                   495 495 I . 2003 AA; 205949 MW;
                 D90779; BAA18881.1;
                                                                                  489
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Q07833;
                                                                                   CONFLICT
                                                                                                                  SEQUENCE
                                                                                                   CONFLICT
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 EMBL;
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 DR DR DR DR SQ ST L L L
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                                                                                     1110 ADSSLIA--GYGSTQTAGYDSNLTAGYGSTQTAREDSSLTAGYGSTSTAGHDSSLIAGYG 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mixino K., Mixino K., Mixino K., Mixino K., Mixino K., Mixino K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.; A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                 522 GNARAGIAQAIATA-GLAQAYLPGKSMMAIGGGTYRGEAGY----AIGYSSISDTG--NW 574
462 ADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVD 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINH-KIZ / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SIMILARITY: TO S.TYPHIMÜRIUM ORF NEAR CYSG (AC P25928).
-i- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92190338; PubMed=1665988;
Moszer I., Glaser P., Danchin A.;
Multiple IS insertion sequences near the replication terminus in
Escherichia coli K-12.;
Biochimie 73:1361-1374(1991).
                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                      YDBA_ECOLI STANDARD; PRT; 2003 AA. P3366; P76087; P76088; P76085; P76859; 01-F8B-1994 (Rel. 28, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein ydba.
                                                                                                                                                         : | : : | : : |1
1226 LTAGYGSNSTAGHESSLIAGYGSTQIAGYE 1255
                                                                                                                                   575 VIKGTASGNSRGH-----FGASASVGYQ 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000237; AAC74483.1; ALT_SEO.
EMBL; AE000237; AAC74487.1; ALT_SEQ.
EMBL; D90778; BAA15009.1; ALT_SEQ.
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MEDLINE=97251357; PubMed=9097039;
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                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562;
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                                                                     Gaps
                                                                                                                          54 DDDLYLEPVQRTAV----VLSFRSDKEGTGEKEGTEDSN-----WAVYFDE----- 95
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                                                                                                                                                                                                                                                                                    214 -EKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373 VDNKGTMTVTDPESIGIQVDG-DQAVVNNEGESAITNGGTGTQINGDDATANNNGKTTVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PTVHLNG-----IGSTLTDTLLNTGATTNVTNDNVTDD------
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                                                                 Indels 207;
Length 2003;
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   Query Match 6.0%; Score 182.5; DB 1; Best Local Similarity 22.8%; Pred. No. 0.1; Matches 158; Conservative 94; Mismatches 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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Bacillus subtilis.
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Matches 151;
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                                                                                                                                                                                                                                                                                             Miwa Y., Fujita Y.;

"Sequencing of a 65 kb region of the Bacillus subtilis genome containing the lic and celloci, and creation of a 177 kb contig covering the gnt-sacxy region.";

Microbiology 142:3113:3123(1996).

-!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM, MOTILITY, SECRETION OR DIFFERENTIATION.
                                                                                                                                                                                                                                                                                                                                                                                               -!- DONAIN: HAS TWO LIGAND-BINDING DONAINS; THE N-TERMINUS, HAS THREE 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED
                                                                                                                                                                                                                                                                                                                                                                                                                                MOTIF REPEATED 31 TIMES.
SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME
SIMILARITY TO THE REPEAT IN E.COLI RHS GROUP OF PROTEINS (RHSA-D).
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                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=168 / BGSC1A1;
MEDLINE=95219088; Pubmed-7704263;
Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;
"Cloning and sequencing of a 29 kb region of the Bacillus subtilis genome containing the hut and wapa loci.";
Microbiology 141:337-343(1995).
                                                                                      "Molecular analysis of three major wall-associated proteins of
Bacillus subtilis 168: evidence for processing of the product of a
gene encoding a 258 kDa precursor two-domain ligand-binding
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OR 32 (POTEWNIAL).
WALL-ASSOCIATED PROTEIN.
3 x 101 AA APPROXIMATE TANDEM REPEATS
1-1.
                                                                                                                                                                                                                                                          STRAIN-168 / BGSCIAl;
MEDLINE-97124196; PubMed-8969509;
Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED, MAY BE RELEASED INTO THE MEDIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 X 21 AA APPROXIMATE TANDEM REP X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4). 2-1.
3acteria; Firmicutes; Bacillus/Clostridium group;
          Bacillus/Staphylococcus group; Bacillus
                                                                MEDLINE=93302506; PubMed=8316082;
                                                                                                                                  Mol. Microbiol. 8:299-310(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, L05634; AAA22883.1; --
EMBL, D31856; BAA06656.1; --
EMBL, D39985; BAA06560.1; --
EMBL, D383026; BAA11683.1; --
EMBL, 299124; CAB15959.1; --
FR; S32920; S32920.
Subtilist; BGI0797; wapA.
InterPro; IPR003305; CBD_6.
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SEQUENCE FROM N.A.
                     NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 KTSLTPKDTSADYKTDSNEI--VYPDVFPNIDLQTFTFNENIKEDLVLHQYNGYNTFTFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 NG------KKTE----VKIGAKTSVIKEKDGKLVTGKGKDENGSSTDEGEGLVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 199;
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11.3%; Pred. No. 0.13;
ve 90; Mismatches 270;
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Conservative
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Escherichia coli
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Mau B., Sha
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                                                                                                                                                                                                                                                                                                                        STRAIN-BRISTOL N2;
MEDLINE-94150718; PubMed=7906398;
MISON R., Alnoscough R., Anderson K., Baynes C., Berks M.,
Milson R., Alnoscough R., Anderson K., Copper J., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          512 NLNNRIDNVDGNARAGIAQAIATAGLAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDT 571
                          559 RYKLHLDGKDG------AELALDPSPVYKNSGGSYATSKNYWIGVSAIFDQ 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 TAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ-----NT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 TVVGADGKNITENSEKKDG-----YNKESKV-----DEANENTKIKSADGSVIET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 NENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG-T 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        '2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 NGDPTVHLNGIGSTLTD-----TLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 NADGTFLRNNTGHKNTDEHLSHNVLDENAQMSIGADGTSHNITNRKGSVGDSHNA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 GVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227; Indels 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 918;
                                                                    ------KGTASGNSRGHF-----GASASVGYQ 597
                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 96.6 kDa protein F59B2.12 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E464FD86B14945DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 181.5; DB
; Pred. No. 0.047;
87; Mismatches 2:
                                                                                                                                                918 AA.
                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 22.1
                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 368:32-38(1994).
                                                                                                                                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                           28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein. SEQUENCE 918 AA; 9
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(Rel.
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                     572 GNWVI-
                                                                                                                                                                           01-FEB-1994
                                                                                                                                                  YMJB_CAEEL
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YMJB_CAEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLNESSIE-SGRKAESRNNTAADTLDSVDANGTVSSSHSKSASGTSLDENHNKTHALQAS 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       434 IEITRNGKNIDIATS----MTPQFSSVSLGA---GADAPTLSVDDEGALNVGSKDANKPV 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
337 AGSNSSKINSASGQSSDLSMVGPNGIKSHSTSNKTDNYALDEANQSAGSISEQIGKNGQR 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     516 LEKN---HEKNSDGT----FKDESKGSNSRVNRTDGGSNLAVG-----SYSVGK- 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto Y., Albo H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Misubhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Sairto N., Sampel G., Satoh Y., Sivasundaram S., Tagami H., Takabashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T., Construction of a contiguous 874-kb sequence of the Escherichia coli-rkl2 genome corresponding to 50.0-68.8 min on the linkage map and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-KIZ / MG1655;
MEDLINE-97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                               287 IKEKDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFE
                                                                                                                                                                                                                290 LKNADGTSMSNSTGNFNNTSYDK----ATAEEVMS-----KKNVNADG-TSSMEASH
                                                                                                                                                                                                                                                                                                       TVTSGTKVTFASG------NG--TTATVSKDDQ------GNITVKYDVNVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RITHNAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQAYLPGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALNVNQLQNSGWNLDSK - - AVAGSSGKV - ISGNVSPSKGKMDETVNI NAGNN - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547 MMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGVSSNE---TIASSNAFNTSD----AESNQFDHLHQKTANG
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DNA Res. 4:91-113(1997).
-!- SUBCELLULAR LOCATION: Outer membrane (Potential).
-!- SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P52143; P76610; P77017; P77019; 01-0CT-1996 (Rel. 34, Created) 01-NOV-1997 (Rel. 34, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Hypothetical outer membrane protein ypjA.
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MEDLINE=97349980; PubMed=9205837;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                     137 KDL-TDLTSVETEKLSFGANGNKVNITSDTKGL-NFAKETAGTNGDPTV-----HLN 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                             214 --EKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTV----- 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 --NVESKDNGKKTEVKIGAKTSVIKEK------------DG--KLVT 296
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                                                                                                                                                                                        Query Match 5.9%; Score 180; DB 1; Length 1569;
Best Local Similarity 20.9%; Pred. No. 0.1;
Matches 140; Conservative 82; Mismatches 227; Indels 222; Gaps
                                                                                                                                                                                                                                                                        G-----ATTNVTNDNVTDD 213
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                                                         EMBL; U36840; AAA79815.1; ALT_SEQ
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Search completed: July 3, 2002, 08:48:50 Job time: 696 sec

Local Match

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RP SEQUENCE FROM N.A.

REDLINE=20175755; PubMed=10710307;

RX MEDLINE=20175755; PubMed=10710307;

RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,

RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,

RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
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                                                                                                      SPECIES-N.meningitidis; STRAIN-PMC21;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R.
Padentification and characterization of a gene en
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ da
EMBL; AF226375; AAF42524.1; --
EMBL; AF226367; AAF42516.1; --
EMBL; AF226370; AAF42519.1; --
EMBL; AF226371; AAF42519.1; --
EMBL; AF226371; AAF42519.1; --
EMBL; AF26374; AAF42519.1; --
EMBL; AF26371; AAF42
       Complete
SEQUENCE
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STRAIN-MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;

MEDLINE-20175756; PubMed-10710308;

Plzza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti,

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

Ratti G., Santini L., Savino S., Jearselli M., Storni E., Zuo P.,

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

Moxon E.R., Grandi G., Rappuoli R.;

Moton E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9JR18 PRELIMINARY; PRT; 591 AA.

G9JR18;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUT-ER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUT PROTEIN).

GNA992 OR NMB0992 OR NHHA.
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                                                                                                                                                      ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                                               GKDKGENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
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548; Conser
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Pred. No. 1.1e
12; Mismatches
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MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Caleotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Ratti G., Santini L., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(200).
EMBL; AF226385; AAF42534.1; -.
SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;
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01-OCT-2000
01-MAR-2001
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Q9JPR7;
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                                                                                         GNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPS
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SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLA
                                      KGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVG
                                                                            GKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPS
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                                                                                                                                              GKDENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFAS
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                        KGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDKGALNVG
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(TrEMBLrel. 15,
(TrEMBLrel. 16,
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Pred. No. 3.9e
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A Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Camanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Camanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Camanducci M., Jennings G.T., Baldi E., Marchetti E., Mora M., Nuti S.,
A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.,
"Identification of Vaccine Candidates Against Serogroup B
"Identification of Vaccine Candidates Against Serogroup B
"Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).

R EMBL; AF226366; AAF42513.1;
C SEQUENCE 591 AA; 62113 MW; 533453CAE5A91EIF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9JPS7
Q9JPS7;
01-OCT-2000
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STRAIN-BZ147
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                                                                                                                                                                                          ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
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  PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN
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(TrEMBLrel.
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Pred. No. 1.1e
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A Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
A Comanducci M., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
A Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
A Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
A Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
A Moxon E.R., Grandi G., Rappuoli R.,
T "Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
R EMBL; AF226378; AAF42527.1; -
C SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
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                                                                                                                              AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGYQW
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16, Last annotation update)
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Pred. No. 7.9e
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Bacteria; Proteobacteria; b
NCBI_TaxID=487;
[1]
SEQUENCE_FROM N.A.
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EMBL; AF226371; AAF42520.1; -.
SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nul Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo I Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H. Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter (Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B
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|KQNTDENTNA----SFTYSLKKELTDLTSVGTEKLSFGANGNKVNITSDTKGLNFAKE 176
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EMBL; AF226376; AAF42525.1; -
EMBL; AF226399; AAF42518.1; -
EMBL; AF226399; AAF42518.1; -
EMBL; AF226399; AAF42518.1; -
           Bacteria; Prote
NCBI_TaxID=487;
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 SEQUENCE FROM
                                Neisseria meningitidis.
Bacteria; Proteobacteria;
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01-DEC-2001 (TrE
OUTER MEMBRANE F
GNA992 OR NHHA.
MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Ario
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora
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peak I.R., Sikhanta Y., Dieckelman M., Moxon R.,
"Identification and characterization of a gene end
membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ data
EMBL; AF157605; AAK68866.1; -
SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CF
                                     SEQUENCE FROM STRAIN-NGH38;
                                                                          Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                                NCBI_TaxID=487;
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01-OCT-2000 (TrEMBLrel 15,
01-OCT-2000 (TrEMBLrel 15,
01-MAR-2001 (TrEMBLrel 16,
00TER MEMBRANE PROTEIN GNA99
         MEDLINE=20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Gi
Comanducci M., Jennings G.T., Baldi L.,
Galeotti C.L., Luzzi E., Manetti R., Ma:
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OUTER MEMBRANE PROTEIN GNA
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SEQUENCE FROM N.A.
STRAIN=NG3/88, AND E
MEDLINE=20175756; Pu
Pizza M., Scarlato V
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Q9JPR9;
01-OCT-2000
                                     Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B. Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecch Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., N Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
   Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AF226382; AF42531.1; -.
SEQUENCE FOR A.
                                                                                                                                     SEQUENCE FROM N.A. STRAIN=NGH36;
                                                                                                                                                                            Neisseria meningitidis
Bacteria; Proteobacteri
                                                                                                                        MEDLINE=20175756;
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                                                                                                                                                                  NCBI_TaxID=487;
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Query Match Best Local Similarity

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Score Pred.

3005; DB 2; No. 2.3e-118;

Length

Moxon

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SEQUENCE FROM
STRAIN=BZ198;
Peak I.R., Sr
                                                                                                                                                                                                                                               Q9JPH7;
Q9JPH7;
01-OCT-2000
01-OCT-2000
01-DEC-2001
                                Meningococcus
Science 287:18
[2]
                                                           SEQUENCE FROM N.A.

STRAIN-BZ198, AND 297-0;

MEDLINE-20175756; PubMed-10710308;

MEDLINE-20175756; PubMed-10710308;

Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.

Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecch

Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., N

Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo

Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin

Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter

Moxon E.R., Grandi G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B

"Tentification of Vaccine Candidates Against Serogroup B
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Bacteria;
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Matches
          MEDLINE-20175756; PubMed-10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
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"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL, AF226359; AAR42508.1; -
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01-OCT-2000 (TrembLrel. 15,
01-MAR-2001 (TrembLrel. 16,
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                                                                                                                                                                                                                                                   STRAIN=2996;
MEDLINE=20175756;
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Bacteria; Proteobacteria;
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Best Local s
Matches 595
STRAIN=B210;
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennir
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennir
"Identification and characterization of a gene encoding
"Identification and characterization of a gene encoding
"membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF157603; AAK68864.1; -
SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Q93QY5;
Q93QY5;
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Bacteria; Proteobacteria;
NCBI_TaxID=487;
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Pred. No. 2.1e-119;
1; Mismatches 2;
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Query Match Best Local Sin Matches 594;

Similarity

99 . 2%;

Score 3021; I Pred. No. 4.9e 1; Mismatches

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Sp_soteria

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Copyright (c) 1993 - 2000 Compugen
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"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., "Identification and characterization of a gene end membrane protein of Neisseria meningitidis."; submitted (JUN-199) to the EMBL/GenBank/DDBJ data EMBL; AF226381; AAF642530.1; -
EMBL; AF157607; AAF68868 1; -
EMBL; AF157607; AAF68868 1; -
EMBL; AF157607; AAF68868 1; -
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
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Query Match

100.0%;

Score 3044;

DB 2;

Length 598;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

July 3, 2002, 08:36:22 ; Search time 104.77 Seconds (without alignments) 633.980 Million cell updates/sec Run on:

3042 1 MNKISRIIWNSALNAWVVVS......TASGNSRGHFGTSASVGYQW 598 US-09-771-382-8 Perfect score: Title:

Scoring table:

Sequence:

747574 seqs, 111073796 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

747574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA2001.

## SUMMARIES

	df				
	Query				,
Score	Match	e Match Length DB I	DB:	ID	Description
3042	100.0	598	20		A surface protein
3042	100.0		22	AAU06178 .	N. meningitidis BZ
3021	99.3		20	AAY23742	A surface protein
3021	99.3		22	AAU06177	N. meningitidis Hl
2948	6.96		20	AAY23739	A surface protein
2948	96.9		22	AAU06179	N. meningitidis BZ
2852	93.8		20	AAY23740	A surface protein
2852	93.8		21	AAY57044	BASB029 amino acid
2852			22	AAU06174	N. meningitidis EG
2821.5	92.8	599	20	AAY23743	A surface protein
21.5		-	22	AAU06176	N. meningitidis H3

Neisseria meningitidis surface proteins useful for treating N. meningitidis infections

WPI; 1999-418754/35. N-PSDB; AAX85790.

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# ALIGNMENTS

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Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.
                                                      A surface protein of Neisseria meningitidis.
         AAY23738 standard; Protein; 598 AA.
                                                                                                                                                                                                   Peak IRA;
                                                                                                                                            98WO-AU01031.
                                                                                                                                                                           (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                            97GB-0026398
                                       08-SEP-1999 (first entry)
                                                                                                                                                                                                   Jennings MP, Moxon ER,
                                                                                             Neisseria meningitidis.
                                                                                                            WO9931132-A1.
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                        AAY23738;
AAY23738
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/label=

.116

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25-JAN-2000; 2000US-0177917.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSK 480
                                                                                                                                                                                                598
                 The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                             541 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW
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Pred. No. 5.6e-176;
Mismatches 0;
Page 91-93; 132pp; English.
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh (AMU06182-AMU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain B210 is 1 of 10 Nhh polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                            ö
                                                                             New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
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100.0%; Pred. No. 5.6e-176;
ive 0; Mismatches 0;
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Best Local Similarity
Matches 598; Conserv
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N-PSDB; AAS09168.
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Conservative

Surface antigen NhhA; meningococcal disease; meningitis vaccine

Neisseria meningitidis strain BZ10.

N. meningitidis B210 surface antigen NhAA polypeptide sequence.

(first entry)

24 -OCT - 2001

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Claim 1; Page 108-110; 132pp; English.
meningitidis infections
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                           PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE
                                                     NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
                                                                                PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                         surface glycoprotein; infection; vaccine;
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N-PSDB; AAX85794.
                                                                                                                                                                                                                                                                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                     1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
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                                                                                                                                                                                                                                                                                                                       PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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Pred. No. 1e-174;
1; Mismatches 3
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594; Conservative
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Matches 594,
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1..50 /label= Cl ^^onte= "Conserved region 1"

Location/Qualifiers

51. 104 /label= V1 /note= "Variable region

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AdMO6182-AAMU6186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding which type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain HIS is lof 10 NhhA polypeptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
           Neisseria meningitidis strain H15.
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N-PSDB; AAS09167.
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/note-195..216 /label= V3 ...e= "Variable region 3"

217..235 /label= C4 /note= "Conserved

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/label= V4 /note= "Variable region 4" 243..598 /label= c5 /note= "Conserved region 5"

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/label= V2 /note= "Variable region

'note= "Conserved region 2"
117..130

'label - C2

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Score 3021; DB 22; Length 598; Pred. No. le-174;

99.3%; 99.3%;

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Query Match Best Local Similarity

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3; Indels
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Matches 594; Conservative
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Surface antigen NhhA; meningococcal disease; meningitis vaccine
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/note= "Conserved region 2"
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/note= "Conserved region 4"
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/note= "Conserved region
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/note= "Variable region
                           Neisseria meningitidis strain BZ198.
                                            Cocation/Qualifiers
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/note= "Variable
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                                                                                                                                                                                                                                                                                                                                                                                   SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGK
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                                                                                                                                                                                                   4;
        Neisseria meningitidis surface proteins useful for treating N.
                                                                                                                                                                              Score 2948; DB 20; Length 594;
Pred. No. 2.7e-170;
2; Mismatches 10; Indels 4
                                   Claim 1; Page 95-97; 132pp; English.
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                                                                                                                                                                              Query Match 96.9%;
Best Local Similarity 97.3%;
Matches 582; Conservative
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                 meningitidis infections
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meningittidis mutant polypeptides of the surface antigon NhhA (AAU06182-AAU06186). The modified or mutant Nhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain BZ198 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention. or New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -

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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                            Neisseria meningitidis surface proteins useful meningitidis infections
                                                     Claim 1; Page 100-101; 132pp; English
   1999-418754/35.
  WPI; 1999-418/24/
N-PSDB; AAX85792
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                    4:
   Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
                    Indels
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Score 2948; DB 22;
Pred. No. 2.7e-170;
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llarity 97.3%;
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                   582;
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93.8%; Score 2852; DB 20; 94.6%; Pred. No. 1.7e-164;
                         5; Mismatches
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                                              Nisseria meningitidis; surface fibril protein; HSF; diagnosis; n; treatment; prevent; antibacterial drug.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
               BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2852; DB 21;
Pred. No. 1.7e-164;
5; Mismatches 23;
                                                                                                                                                                /note= "Encoded by AATC"
                                                                                                                                                                                                                                                                                                                                   SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Fig 2; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%;
94.6%;
                                                                                                                                                                                                                                                                 99WO-EP03255.
                                                                                                                                                                                                                                                                                                  98GB-0010276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.8
Best Local Similarity 94.6
Matches 566; Conservative
                                                                                               Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receiving the protein.
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-053103/04.
N-PSDB; AAZ39864.
                                                                                                                                               Misc-difference 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594 AA;
                                                                                                                                                                                                W09958683-A2
                                                                                                                                                                                                                                                                 07-MAY-1999;
                                                                                                                                                                                                                                                                                                13-MAY-1998;
                                                                                                                                                                                                                                .8-NOV-1999
                                                                 Infection;
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                                              BASB029;
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                                                                                                                                                                                                                The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhA (AAU06186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.
                                                                                                                                                                                                                                                                                                                               The present sequence representing the wild type surface antigen Nhh
from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences
(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGN 360
                                                                                                                                                             or
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gttatvskddqgnitvmydvnvgdalnvnqlqnsgwnldskavagssgkvisgnvspskg
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                               NhhA surface antigen polypeptides and polynucleotides from
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2852; DB 22;
Pred. No. 1.7e-164;
5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                5.
                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                           93.8%;
94.6%;
                                            25-JAN-2000; 2000US-0177917.
                      25-JAN-2001; 2001WO-AU00069
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                  (UYQU ) UNIV QUEENSLAND
                                                                                         Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                                                                                                    present invention.
                                                                                                                                                                                             Claim 9; Fig 1; 91pp;
                                                                                                               WPI; 2001-488774/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                           N-PSDB; AAS09164.
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 02-AUG-2001
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Best Local S:
Matches 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPVORTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                   541 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.8%; Score 2821.5; DB 20; Length 599; 92.7%; Pred. No. 1.2e-162; ive 13; Mismatches 30; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis surface proteins useful for treating meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                                   surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Indels
                                                                                                                                                                                                                                                                                                                                                                       A surface protein of Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 114-115; 132pp; English.
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                                                                                                                                                                                                                                AAY23743 standard; Protein; 599
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                                                                                                                                                                                                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoreactive peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                         (first
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N-PSDB; AAX85795.
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                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09931132-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-1998;
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25-JAN-2000; 2000US-0177917 25-JAN-2001; 2001WO-AU00069

WO200155182-A1. 02-AUG-2001 UYQU ) UNIV QUEENSLAND

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Peak IRA,

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                                                                                                                                                                                                           KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASG
                                                                        DPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT
                                 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG
                                                                                                 NGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                 GKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGS
                                                                                                                                                                  KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQ
                                                                                                                                                                                                  540 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW
                                                                                                                                                                                                                                                                                                                             Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                             N. meningitidis H38 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                      "Conserved region 1"
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/note= "Conserved region
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/note= "Variable region
132,.195
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/note= "Variable region
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis strain H38
                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Variable
                                                                                                                                                                                                                                                           AAU06176 standard; Protein; 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= C4
                                                                                                                                                                                                                                                                                             (first entry)
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/label= Cl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh (AAN06182-AAN06186). The modified or mutant Nhhh polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain 188 is 1 of 10 Nhha polypeptide sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG 179
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                                                                                                                                                                                                                                        Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL
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Pred. No. 1.2e-162;
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92.7%;
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Best Local Similarity
Matches 555; Conserv
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24-SEP-1999
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Matches 550;
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                                                                                                                                                                                                                      BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
                                        540
421 gkmdetvninagnnieitrngknidiatsmtpqfssvslgagadaptlsvddkgalnvgs 480
                                                                         KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide from neisseria meningitidis useful for diagnosis, thment or prevention of bacterial infections in mammal
                                                              540 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW
                                                                                                                                                                                                   BASB029 amino acid sequence from N. meningitidis strain H44/76.
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                                                                                                                                    AAY57045 standard; Protein; 591
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                                                                                                                                                                               (first entry)
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N-PSDB; AAZ39865.
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the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASBO2 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416
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                                                                                                                                                                                                                                                                                                                                                                                                                  58 YLEPVQRTAVVLSFRSDKEGTGEKEGT-EDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
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                                                                                                                                                                                                                                                         21; Length 591;
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                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                         Score 2732.5; DB 3
Pred. No. 2.8e-157,
8; Mismatches 29,
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91.4%;
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                                                                                                                                                            receiving the protein.
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58 YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
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Best Local Similarity 90.7%; Pred. No. 2.6e-156;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps
                                                                                              meningtidis which is approximately 62 kba. The N. meningtidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningtidis infection in humans. The N. meningtidis surface glycoproteins can also be used to in the form of vaccines. The protein in humans, especially in the form of vaccines. The proteins and antibodies can also be used to be used to identify immunoreactive peptides.
                  VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                  LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGY
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                                                                                                                                                                                                                                                                                                                                                                                     surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                    A surface protein of Neisseria meningitidis.
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N-PSDB; AAX85798.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New protein and its nucleotide sequence, useful in vaccines or diagnostic compositions for treating and/or preventing Neisseria {\sf vac}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2716.5; DB 20; Lung-
Pred. No. 2.6e-156;
'''.amatches 28; Indels
                                                                                                                                                                                                                                                        Scarlato
                                                                                                                                                                                                                                                        Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                        Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 62; 123pp; English.
bacterial infection; treatment,
                                                                                                                                                        98GB-0022143.
98GB-0000760.
98GB-0019015.
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                               Neisseria meningitidis.
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Best Local Similarity
Matches 546; Conserv
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                                                             W09936544-A2
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/label= C3

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61 yldpvqrtvavlivnsdkegtgekekveensdwavyfnekgvltareitlkagdnlkikg 120
           GKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTF
                                                                                                        ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                               PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                                     TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
                                                         GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                       VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQALATAG
                                                                                                                                                                                                                                                                                N. meningitidis PMC21 surface antigen NhhA polypeptide sequence
                                                                                                                                                                                                                                                                                            Surface antigen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                                                                                                                                                                                                                                   /note= "Predicted mature protein, specifically
claimed in claim 12"
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/label= Cl
'...te= "Conserved region 1"
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/note= "Conserved region 2"
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/note= "Variable region 2"
125..188
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                                                                                                                                                                                                                                                                                                                         1.51
/label= Signal_peptide
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/label= Mature_NhhA
                                                                                                                                                                                                                                                                                                        meningitidis strain PMC21
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/label= v1
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The present invention relates to the isolation of novel Neisserla meningitidis mutant polypeptides of the surface antigen Nhh AAMUGE182-AAWUGE186). The modified or mutant Nhh polypeptides are characterised by deletions of non-conserved maino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain PWC21 is 1 of 10 Nhh polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG
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"Conserved region 3"
                                                                          /note= "Variable region 3"
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/note= "Conserved region
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/note= "Variable region
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/note= "Conserved
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                                              /label= v3
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Best Local Similarity 90.77
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  /note= "C
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296
               GKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSGTKVTF 356
                               PSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN 476
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Search completed: July 3, 2002, 08:36:23 Job time: 319 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein – protein search, using sw model

July 3, 2002, 08:37:08; Search time 39.66 Seconds Run on:

(without alignments)
368.293 Million cell updates/sec

US-09-771-382-8 3042 1 MNKISRIIWNSALNAWVVVS......TASGNSRGHFGTSASVGYQW 598 Perfect score: Sequence:

**BLOSUM62** Scoring table:

231628 segs, 24425594 residues Gapop 10.0 , Gapext 0.5

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_AA:\* Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Appli	Appli	Appl ,	, Appl	Appli	Appl i	Appl i	App1	, Appl	, Appl	, Appl	App]	Appli	Appli	, App]	, Appl	, App]	, App]				Appli	, Appl	, Appl	, Appl	7	
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	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	
SUMMARIES		77-155-5	-09-669-974-5	77-155-13	US-09-669-974-13	77-155-7	US-09-669-974-7	-377-155-9	US-09-669-974-9	77-155-15	US-09-669-974-15	77-155-21	US-09-669-974-21	US-09-377-155-2	US-09-669-974-2	-377-155-11	US-09-669-974-11	77-155-17	US-09-669-974-17	-377-155-19	US-09-669-974-19	77-155-33	13-942-4	69-974-33	68-347-47	-09-268-347-36	-08-409-995-6	
SUMM	ID	US-09-3	9-60-Sn	US-09-377-15	9-60-SN	US-09-377-155	9-60-SD	US-09-3	9-60-SN	US-09-377-15	9-60-SN	US-09-377-15	9-60-Sn	ns-00-3	9-60-Sn	ns-09-3	9-60-Sn	US-09-377-15	9-60-Sn	US-09-3	9-60-sn	US-09-377-155	US-08-913-	-699-60-SN	US-09-268-	US-09-2	US-08-4	
	DB	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	4	7	4	4	4	-	
	Length	598	598	598	598	594	594	594	594	599	599	591	591	592	592	591	591	592	592	589	589	2353	2353	2353	2354	2411	607	
d	Query Match	100.0	100.0	99.3	99.3	96.9	6.96	93.8	93.8	92.8	92.8	89.3	89.3	89.1	89.1	88.9	88.9	87.4	87.4	86.0	86.0	43.1	43.1	43.1	43.1	42.3	40.9	
	Score	3042	3042	3021	3021	2948	2948	2852	2852	2821.5	2821.5	2716.5	2716.5	2709	2709	2705.5	2705.5	2658	2658	2616.5	2616.5	1312.5	1312.5	1312.5	1311.5	1286.5	1245	
	Result No.	1	7	e	4	2	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	

Sequence 6, 1	Sequence 4,	7,7	Sequence 2, Appl	Sequence 2, Appl	Sequence 32,	Sequence 44, App	Sequence 5, A	Sequence 5, Appl	Sequence 5, A	Sequence 15,	Sequence 26,	Sequence 24,	Sequence 30,	Sequence 28,
US-08-913-942-6 US-08-409-995-4	US-08-685-467-4 US-09-268-347-32	US-08-409-995-2	US-08-685-467-2	US-08-913-942-2	US-09-669-974-32	US-09-268-347-44	US-08-409-995-5	US-08-685-467-5	US-08-913-942-5	US-08-913-942-15	US-09-268-347-26	US-09-268-347-24	US-09-268-347-30	US-09-268-347-28
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607 1912	1912	1098	1098	1098	1098	1098	658	658	658	619	619	1002	1004	1104
40.9	40.9	34.6	34.6	34.6	34.6	34.6	34.2	34.2	34.2	33.0	33.0	25.0	24.8	23.1
1245	1245	1054	1054	1054	1054	1054	1040	1040	1040	1004.5	1004.5	762	753	703
28	30	32	33	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
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100.0%; Pred. No. 4.5e-239;
tive 0; Mismatches 0;
                                                                                                                                                               APPLICANT: PERK, Ian Richard Anselm APPLICANT: PERK, Ian Richard Anselm APPLICANT: PENNINGS, Michael Paul APPLICANT: PENNINGS, Michael Paul International Control of 
                                                                               Sequence 5, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
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LENGIH: 598
RESULT 1
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Pred. No. 2.3e-237;
1; Mismatches 3;
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CURRENT APPLICATION NUMBER: 1099-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
LENGTH: PALCHING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
LENGTH: 598
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; Sequence 13, Application US/09377155
; Patent No. 6197312
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US-09-377-155-13
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4; Conservative
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Best Local Simi
Matches 594;
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; Pred. No. 4.5e-239;
0; Mismatches    0;
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Petent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TILLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILLE REPERENCE: 065064/0128
CURRENT FILING DATE: 2000-09-26
PRIOR PELICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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US-09-669-974-5
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Best Local Similarity 100.0%;
Matches 598; Conservative 0
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   GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 420
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Pred. No. 2e-231;
2; Mismatches 10;
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CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
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Patent No. 6197312
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97.38;
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Best Local Similarity
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Pred. No. 2.3e-237;
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                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09669974 Patent No. 6333173
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94.6%; Pred. No. 1.2e-223;
11ve 5; Mismatches 23;
                                                                                                                                                                         GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PERK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: WONN, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCHIN Ver
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CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOUTHARE: PATENTIN VET: 2.0
                                                                                                                                                                                      Sequence 7, Application US/09669974 Patent No. 6333173
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US-09-669-974-7
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Best Local Similarity 97.3
Matches 582; Conservative
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                                    1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
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CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APLICATION NUMBER: GB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 599
                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANFIGEN
FILE REFERENCE: 065064/0128
                                                                                                                                         Sequence 15, Application US/09377155 Patent No. 6197312
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Best Local Similarity
Matches 555; Conserv
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Pred. No. 1.2e-223;
5; Mismatches 23;
                                                                                                                                                  Sequence 9, Application US/09669974
Patent No. 6333173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
IIIE REPERENCE: 065064/0128
CURRENT FILLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REPERENCE: 065064/0128
CURRENT FILIAG DATE: 2000-09-26
PRIOR PLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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Best Local Similarity 94.6%;
Matches 566; Conservative
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SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                         US-09-669-974-9
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 9
LENGTH: 594
                477
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 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89.3%; Score 2716.5; DB 4 90.7%; Pred. No. 1.3e-212;
                                                                                                                                  APPLICANT: PEAK, Ian Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: MOXON, E. Richard Paul APPLICANT: MOXON, E. Richard Paul TILE OF INVENTION: NOVEL SURPACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
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                                                                                   Sequence 21, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT CRGANISM: Neisseria meningitidis US-09-377-155-21
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                     GENERAL INFORMATION:
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Matches 546;
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LENGTH: 591
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                                                                                                                               GENERAL INCORNATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
ITILE OF INVENTION: NOVEL SURPACE ANTIGEN
FILE REFERENCE: 06504/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
SPRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
                                                                                                 Sequence 15, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Neisseria meningitidis US-09-669-974-15
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LENGTH: 599
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61 LYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKKGVLTAREITLKAGDNLKIK 120
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530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY
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llarity 90.4%; Pred. No. 5.1e-212;
Conservative 12; Mismatches 30;
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: BUNINGS, Michael Paul
APPLICANT: BUNINGS, Michael Paul
TITLE OF INVENTION: ROUEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT RAPLICATION NUMBER: U$/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-11-12
                                                                                                                                Sequence 2, Application US/09377155
Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Neisseria meningitidis US-09-377-155-2
                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin ver. 2.0 SEQ ID NO 2
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Best Local Similarity
Matches 545; Conserv
                           QW 598
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                                                                                                                      GENEKAL INFUGRALIAN:
GENEKAL INFUGRALIAN:
APPLICANT: PEAK, IAN Richael Paul
APPLICANT: JENNINGS, Michael Paul
TITLE COF INVENTION: E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-108-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
SPRIOR FILING DATE: 1998-12-14
SPRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SCOTTWARE: PATENTIN VET. 2.0
SEQ ID NO 21
LENGTH: 591
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                                                                                    Sequence 21, Application US/09669974
Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Neisseria meningitidis US-09-669-974-21
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Best Local Similarity 90.7%;
Matches 546; Conservative 13
                                                                                                                 GENERAL INFORMATION:
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                                                                     US-09-669-974-21
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APPLICANT: PEAK, IAN Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
TITLE OF INVENITION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
SOFTWARE: PATCHIN VOR: 2.0
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; Patent No. 6197312
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US-09-377-155-11
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LENGTH: 591
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PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLV
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                                                                                                                                                                                             CHERCANT: DEDAK, IAN Richard Anselm APPLICANT: DENNINGS, Michael Paul APPLICANT: DENNINGS, Michael Paul APPLICANT: DENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN FILE REFERENCE: 065064/0128

CURRENT FILING DATE: 2000-09-26

CURRENT FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1998-12-14

PRIOR FILING DATE: 1998-12-14

PRIOR FILING DATE: 1997-12-12

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 2: SEQ ID NOS: 33
                                                                                                                                                    Sequence 2, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Neisseria meningitidis
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Best Local Similarity
Matches 545; Conserv
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US-09-669-974-2
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53/ LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGY	530 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY 589
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Search completed: July 3, 2002, 08:37:10 Job time: 336 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on:

July 3, 2002, 08:38:17; Search time 58.79 Seconds (without alignments) 977.401 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-771-382-8 3042 1 MNKISRIIWNSALNAWVVVS......TASGNSRGHFGTSASVGYQW 598

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	adhesin NMB0992 [1	probable surface f	adhesin homolog HI		probable autotrans	surface protein XF	probable adhesin Z			surface-exposed ou	hypothetical prote	n,	high-molecular-wei	probable autotrans		Aida-I adhesin-lik	probable adhesin 2	probable adhesin P	hemolysin A - Serr	S-layer protein -	adhesin	surface-array prot		ydek pro	hypothetical		hypothetical	hvnothetical prote
SUM	ID	G81133	A81888	164138	D82671	AC0976	A82615	A86036	н91188	AH0110	C82672	G64964	AF0394	A43855	AD0123	T31105	D90803	н85611	H83135	A28182	T03415	S28634	A56143	AD0548	A64905	B98047	B85547	F90696	F85809
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199	199	199	198.5	198	197	195	195	192.5	192.5	192	191.5	191.5	191	190.5	190.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

357 ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS 416

δy

Db 351 ASGRCTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSRAVAGSSGKVISGNVS 410  Qy 417 PSRGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN 476	QY         411 ISGNVSPSKCKMDETVNINACNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVD 470           Db         405 ISGNVSPSKCKMDETVNINACNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVD 464           QY         471 DEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQ 530           QY         455 DEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQ 524           QY         531 AIATAGLAQAYLPGKSMALGGGTYRGEAGYAIGYSGNIGTGSSISDTGNWVIKGTASGNISRGHFGF 590           Db         525 AIATAGLVQAYLPGKSMALGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNISRGHFGF 584           QY         591           RESULT         3
SULT 2 1888 obable surf Species: Ne Species: Ne Species: Ne Species: Ne Species: Ne Parkhill, J Parkhill Comp Reference n Status: pre Residus: pre Residus: pre Residus: pre Residus: pre Residus: pre Residus: I Cross-refer Experimenta Genetics:	defined by the conservative of strain Rd KW20)  164138  adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)  C;Saccies: Haemophilus influenzae C;Saccession: 164138  R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage R;Fleischmann, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weldman , D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995 A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Hitle: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630 A;Accession: 164138 A;Accession: 164138 A;Accession: 164138 A;Accession: 164138 A;Accession: 164138 A;Grass-references: GB:U32846; GB:L42023; NID:91574588; PID:91574589; TIGR:HI1732 Query Match Best Local Similarity 46.2%; Pred. No. 6.6e-25; Matches 150; Conservative 39; Mismatches 90; Indels 46; Gaps 9;
Query Match 82.9%; Score 2521; DB 2; Length 592; Best Local Similarity 85.5%; Pred. No. 3.4e-121; Matches 520; Conservative 16; Mismatches 46; Indels 26; Gaps 8;	OY 1 MNKISKIIWNSALNAWVVVSELTRNHTKRASATVATAVLLFATVQANATDDDDLYLE 60      ::     ::
OY 1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL 59	Qy 61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAG-AITLKAGDNLKIKQNTN 119 ::: ::: ::: :::: :::: :::: ::: ::: :::
O EYQKIYYVESTSDAEDGEAGA	120 ENINEAN NESSELISENDE SETEMBERGAN ON WALLS DE NEW ALL SELECTION OF THE SETEMBERGAN OF THE SET SETEMBERGAN OF THE SETEMBERGAN
QY         173 ETAGTNGDPTVHLNGIGSTLEDTLLNTGATTNVTNDNVTDDEKRAASVKDVLNAGWNIK 232	QY         233 GVKPGTTASDNVDEVRTYDTVELSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDG         292               ::
OY 291 DGKLVTGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRWTTTANGOTGQADKFETVTS 350	RESULT 4 B02671 Surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c) C. Species: Xylella fastidiosa C. Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C. Accession: D82671 R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seg

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probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi C; Dapecies has also been called Salmonella typhi C; Davecies to Hovo-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C; Accession: AC0976 R; Parkhill, J; Dougan, G; James, K.D; Thomson, N.R.; Pickard, D.; Waln, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A; Reference number: AB0502; PMID:11677608
A; Accession: AC0976
A; Accession: AC0976
A; Accession: AC0976
A; Residues: 1-1107 < PARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AL513382; PIDN: CAD03303.1; PID: 916504923; GSPDB: GN00176 C; Genetics:
NDSSFTYSLKKDLTDL-TSV-----ETEKLSFGAN--GNKVNITSDTKGLNFAKE 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQN-- 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              286 TNLAAGTLAADSTDAVNGSQLYETNQKVDQNTSAIADINTSITNLSSDNLSWNETTNSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KGVKPGTTASDNVDFV - - - RTYDT - - - - - - VEFLSADTKTTTVN - - - - - VESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 TAGTNGDPTVHLNGIGSTLTDTL--LNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.8%; Score 390; DB 2; Length 1107; Best Local Similarity 21.8%; Pred. No. 2.3e-12; Matches 182; Conservative 114; Mismatches 262; Indels 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EGLV----TAKEVIDAVNKA----GWRMKTTTANGQTGQ-
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                                                                                                                   -----NIEITRNGKNI-----
                                                                                        GYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW
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                                                                                                                               A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-2059 <-SIM>
A; Cross-references: GB: AE003982; GB: AE003849; NID: g9106554; PIDN: AAF84338.1; GSPDB: GN001
A; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
R; Simpson, A.J. G; Renach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Psinones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm 3. Netto: Ferritat to GenBank, V.M. Berro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm 3. D.; Junqueira, M.L.; Remper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madelara, A.M.B.N.; Mare, M.R.F.; Marion, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jt.V. V.E.; de Sa, R.C.; Santelli, R.V.; Savasak A; Althors: ad Silva, A.C.R.; da Silva, F.R.; de Salva, S.C.; Sartelli, R.V.; Savasak A; Refrigues, V.; Martins, M.A.; silva Jr., W.A.; ad Silveir A; Contents: annotation
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1689 SHVAVGMADTDAVNVSQLKQAVQSVTVKATRYYSTNDGGTQGGNYDGDGATGSKAIAAGV 1748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAVNFSOLK---SVSEAVDKGWTLTASGANGSKVVSGGTVDLKNTDGNLAISKSGDSNDV 1630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::|::| |::| |: | |::||| |: || |::||| |:||| |:||| |:||| |:||| |:||| |:----navaigngsva-----dransvsvgsggser--qvtnvaagtadtdadtdavnvsqln 1964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKGLNFAKETA----GTNGDPTVHLNGI-----GSTLTDTLLNTGA--TTNVT----N 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEFLSADTK-----TTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGEN-- 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KRVLKAGAITLKAGD-NLKIK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q--NTNE---NTNENTNDSSFTY---SLKKDLTDLTS---VETEKLSFGANGNKVNITSD 164
           A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: D82671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IEDVFKITKGDSASSVKG-------MGVNAMAIGTNAAVSGTESVALGKNTNVSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----KAVAGSSGKVISGNVSPSKGKMDETVNINA---GNNIEITRN-----GKNIDIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----GSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTG-----QADKFETVTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----QNNG-----QNSGMNLDS-----DALNVIQL----QNSGWNLDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.2%; Score 403; DB 2; Length 2059; 24.7%; Pred. No. 1.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1e-12;
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  Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Matches 172;
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OY 206 TNDNVIDDEKKRAASVKDVLNAG-WNIKGVKPGTTASDN 243    :     :     :	Db 1004 Qy 468 Db 1046 Qy 516 Qy 516 Db 1104 Qy 572 Db 1164	RESULT 7 A86036 probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93 CrSpecies: Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: A86036 C;Accession: A86036 C;Accession: A86036 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: A86036 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-1588 <sto> A;Cross-references: GB:AE005174; NID:912518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP: A;Cenerics: A;Gene: 25029</sto>	Ouery Match  12.0%; Score 365; DB 2; Length 1588;  Best Lacal Similarity 25.0%; Pred. No. 6.9e-11;  Matches 144; Conservative 81; Mismatches 252; Indels 98; Gaps 19;  QY 111 NLKIKONTNENTNENTROSFTYSLKELDLTSVETEKLSFGANGNKUNT 162
Db   814   NVAAGSADTDAVNVGQLKVTDAQVSRNTQSITNLNTQVSNLDTRVTNIENGIGDIVTTGS   873	RESULT 6 A82615 surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c) C; Species: Xylella fastidiosa C; Species: 18-4ug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Accession: A82615 R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent A; Title: The genome sequence of the plant pathogen Xylella fastidiosa. A; Reference number: A82515; MUID:20365717 A; Note: for a complete list of authors see reference number A59328 below A; Astatus: preliminary A; Molecule type: DNA	A.Cross references: GB.AE004017; GB.ED003849; NID:99107083; PIDN:AAF84783.1; GSPDB:GN001 A.Experimental source: strain 9a5c A.Stangon, A.JG.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Ariangon, A.JG.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Briones, M.R.S.; Bueno, M.R.P.; Camargo, J.S.; Franca, A.J.S. submitted to GenBank, June 2000 J.D.; Junquaira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr chado, M.A.; Madeira, A.M.B.N.; Madeira, J.P.; Marcino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsub, M.C.; de Oliveira, R.C.; Bilmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.M.; Silva, A.C.R.; da Silva, R.S.; Santelli, R.V.; Sawasak A.Athhors: a Silva, A.C.R.; da Silva, R.A.; Silva, A.M.; Silva, M.C.; Rolado, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z. A.Gontents: annotation C.Genetics: A.Genetics: A.Genetic	Ouery Match  12.6%; Score 383.5; DB 2; Length 1190;  Best Local Similarity 24.6%; Pred. No. 5.5e-12;  Matches 169; Conservative 89; Mismatches 226; Indels 203; Gaps 30;  Qy 47 VQANATDDDDLXLEPVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITL 106  1   1   1   1   1   1   1   1   1   1

Db 1315 DAQVSQNTGSITNLDNRYTNLDSRYTNIENGIGDIVTTGSTKYFKTNTDGVDASAQGKDS 1374  Qy 401 KAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFS 454	on, N.R.; ( T.; Cron. M.; Skelt, nia pestis 21470413; BIDN:CAC89	Matches 144; Conservative 87; Mismatches 254; Indels 156; Ga datches 144; Conservative 87; Mismatches 254; Indels 156; Ga 27 TKRASATVATAVLATLLEATVQANATDDDDLYLEPVQRTAVVLSFRSDK	DD 191 QVTAAGATAIGSAAQAGGAOSLALGAGAVTSQANSIALGAASINTYGAQSSYSAYA 246  QY 180DPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNA 227  18
Db 1195 TEEDSLAVGTDSLAMGAKTIVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVNSIAIG 1254  Qy 303 NGSSTDEGEGLVTAKEVIDAVNKAGWRWKTTTANGQTGQADKFETVTSGTKYT 355	RESULT 8 H91188 probable adhesin EC\$4480 [similarity] - Escherichia coli (strain O157:H7, substrain EC\$56cies: Escherichia coli C; Species: Escherichia coli C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001 C; Accession: H91188 R; Hayashi, T; Makino, K; Ohnishi, M; Kurokawa, K; Ishii, K; Yokoyama, K; Han, Gasawara, N; Yasunaga, T; Ruhara, S; Shiba, T; Hattori, M; Shinagawa, H. DNA Res. 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gA; Accession: H91188 A; Accession: H91188 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1588 chav.	A;Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:g13363955; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: ECs4480  Query Match Query Match 12.0%; Score 365; DB 2; Length 1588; Best Local Similarity 25.0%; Pred. No. 6.9e-11; Matches 144; Conservative .81; Mismatches 252; Indels 98; Gaps 19; Qy 111 NLKIKONTNENTNENTNENTNESFTYSLKKDLTDLTSVETEKLSFGANGNKVNIT 162                                   Db 1025 NMMIEQNT-QIINQLAGNTDATY-IQENGAGINYVRTNDDGLAFNDASAQGVGATAIGYN 1082	Qy         163 SDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNTGA-TTNVTNDNVTDDEK         215           Db         1083 SVAKGDSSVAIGQGSYSDVDTGIALGSSSVSSRVIAKGSRDTSITENGVVIGYDTTDGEL         1142           Qy         216 KRAASVKDVLNAGMNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNNES         269           1143 LGALSIGDDGKYRQIINVADGSEAHDAVT-VRQLQNAIGAVATTPTKYFHANS         1194           Qy         270 KDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGE

Db 204 KSQLDGVTASVNDVAASVKTIALTNQVTGSSVASAGKESTAIGSGAQAVADN 256  Qy 251 DTVEF		Oy 578GTASGNSRGHFG-TSASVGY 596  Db 656 GEHGVALGTDAGVSGRDSIALGY 678  RESULT 11  G64964  hypothetical protein b2000 - Escherichia coli C;Specias: Escherichia coli C;Specias: L2-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001 C;Accession: 664964  R;Blattner, F.R.; Plunkett III, G; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A; Rsos, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617 A;Accession: G64964 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA	A; residues: 1-104 cALATO AND ASTRONOMY A; TOO A A; TOO AND A; TOO A A; COO A A; Experimental source: strain K-12, substrain MG1655 C; Keywords: nuclectide binding; P-loop F; 683-690/Region: nuclectide binding motif A (P-loop) F; 683-690/Region: nuclectide binding motif A (P-loop)  Query Match Best Local Similarity 22.7%; Pred. No. 0.00072; Matches 140; Conservative 64; Mismatches 255; Indels 158; Gaps 25; Qy 1 MNKISRIIWNSALNAWWVVSELTRNHTKRASATVATAVLLFATVQANATDDDLYLE 60 III
Qy   401 KAVAGSSGKVISGNVSPSKCKMDETVNINAGNNI-EITRNGKNIDIATSMTPGFSSVS 457   1   1   1   1   1   1   1   1   1	RESULT 10  C82672  Surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a c; Species: Xylella fastidiosa  C; Species: Xylella fastidiosa  C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000  C; Accession: C82672  R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000  A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.  A; Neterence number: A82515; MUID:20365717  A; Note: for a complete list of authors see reference number A59328 below.  A; Status: preliminary  A; Molecule type: DNA	A; Residues: 1-1004 <sim> A; Cross references: GB:AE00381; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001 A; Cross references: GB:AE00381; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001 A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Pstiones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laign Gado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marrino, C.L.; Marques, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P. Rodrigues, V.; Rosa, A.J. de M.; de Rosa J.V., V.E.; de Saltvai, R.C.; Palmieri, D.P. A.Authors: da Silva, A.C.R.; da Silva, A.M.; Silva J., W.A.; da Silvein M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.A.; A.Genetics: Annotation C; Genetics: A; Gene: XF1516</sim>	Ouery Match  Best Local Similarity 21.7%; Score 241; DB 2; Length 1004;  Best Local Similarity 21.7%; Pred. No. 7.9e-05;  Matches 161; Conservative 101; Mismatches 265; Indels 216; Gaps 35;  QY 2 NKISRIIWNSALNAWVVSELTRNHTRRASATVATALLEATVQANAT 52

Db 654 KGSVIFAGVADHIINNNG-TLDGTLTTGAGNDTLVLDSSSQSNDVINLGDGNN 705  Qy 434 IEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAP 493	i ducreyi  con 22-Oct-1999 #text_change 22-Oct-1999  con 22-Oct-1999  con 22-Oct-1999  con 22-Oct-1999  con 22-Oct-1999  con 23-Oct-1999  con 23-Oct-1999  con 23-Oct-1999  con 24-Oct-1999  con 24-Oct-	TAVLATILEATVQANATDDDDL-YLEPVQRTAVY
OY 325 KAGWRMTTTANGQTGQADKFETVTSGTKVTFASGNGTTATVSK 368 : :	RESULT 14 AD0123 Probable autotransporter protein yapH [imported] - Yersinia pestis (strain CO92) C; Species: Versinia pestis C; Species: Versinia pestis C; Date: 02-Nov-2001 #text_change 02-Nov-2001 C; Accession: AD0123 R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies, P.; Dougan, G.; I. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-577, 2001 A.Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360 A.Stetus: preliminary A; Molecule type: DNA A; Residues: 1-3705 <rur> A; Residues: 1-3705 <rur> C; Genetics:</rur></rur>	Ouery Match Ouery Match Best Local Similarity 21.0%; Pred. No. 0.0079; Matches 131; Conservative 83; Mismatches 237; Indels 172; Gaps 27; Matches 131; Conservative 83; Mismatches 237; Indels 172; Gaps 27;  Oy 36 TAVLATLEATVOANTDODDLYLEPVORTAVVLSFRSDKEGTGERECTEDSNWAV 91

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463	926	503	986	544	104]	10	32
415VSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGAD 463	876 SNSLLDISVAEGKKTFNNGTIESGKNLNITNTGAFLNVDNATIRSFGVLNI 926		927 TSTGNVSNNGTLISNERLNITSAANFINESNGTVMSNGLLNIIAKQGNITNKNLIASRQQ 986	504 AQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQAYLPG	987 INLTAVADNITNDSNISNKIAVLHSLGNISLNSKDQVYNLGELYAGNNISVKAHQ 1041	545KSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGY 596	
415	876	464	927	504	987	545	1042
Qy	Db	ογ	qa	٥y	qq	ογ	QQ

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OM protein - protein search, using sw model

July 3, 2002, 08:48:50 ; Search time 29.79 Seconds (without alignments) 777.250 Million cell updates/sec Run on:

US-09-771-382-8 3042 1 MNKISRIIWNSALNAWVVVS......TASGNSRGHFGTSASVGYQW 598 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Dèscription			Q03155 escherichia	P32051 escherichia	P15921 rickettsia	P16466 proteus mir	P33666 escherichia	Q52657 rickettsia	Q53047 r outer mem	ŗ	P25927 salmonella	Q9kka3 r outer mem	P18127 xanthomonas	P34487 caenorhabdi		Q07833 bacillus su	P52143 escherichia		P35827 campylobact			P19570 bacillus sp	Q53020 r outer mem	_	_			t amylopu	Q08860 shigella fl	-	4	59 salmonel	Q06982 salmonella
SUMMARIES	ID	AG43 ECOLI	HLYA_SERMA	AIDA_ECOLI	YDEK_ECOLI	OMPA_RICRI	HLYA_PROMI	YDBA_ECOLI	OMPA_RICCN	OMPB_RICRI	120K_RICRI	BIGA_SALTY	OMPB_RICCN	ICEN_XANCT	YMJB_CAEEL	OMPB_RICTY	WAPA_BACSU	YPJA_ECOLI	OMPB_RICJA	SLAP_CAMFE		SLAP_BACST	GUN3_BACS4	OMPB_RICPR	YS89_CAEEL	Y741_CHLMU	IGAO_HAEIN	IGA2_HAEIN	APU_THETU	FLIC_SHIFL	SLAP_CAUCR	HXA2_HAEIN	FLIC_SALNA	FLIC_SALRO
	DB	-	٦	Н		-	Н	Н	٦	Н	Н	Н	-	7	٦	ч	7	-	7	7	-	П	П	_		Н	Н	-	Н	Н	Н	П	П.	-
	Query Match Length	1039	1608	1286	1325	2249	1577	2003	2021	1654	1300	1953	1655	1567	918	1645	2334	1569	1656	933	671	1228	825	1643	2329			_	1861	550	1025	2	504	504
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	Score		211	209	203.5	199	195	190.5	189	185.5	185	185	184.5	182	181	181	180.5	180	178.5	177.5	171	169	168		167.5	166	165		164.5	164	16	163.5	161	161
	Result No.	П	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q01714 rattus norv P45355 haemophilus Q9rb65 chlamydia p P04949 escherichia Q06983 salmonella P20469 pantoea ana Q06669 salmonella Q06971 salmonella P06620 pseudomonas P56867 deinococus	
SPI_RAT HXA3_HAEIN PWIO_CHLPN FLIC_ECOLI FLIC_SALSE ICEA_PANAN FLIC_SALBU FLIC_SALBU ICEN_PSESY HPII_DEIRA	VAC3_HELPY MRSP_STAAU
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788 917 928 497 504 1322 504 504 1200 948	1310 1637
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34 35 37 37 38 38 44 40 42 33	4 4 5 5

## ALIGNMENTS

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121 NINENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180
                                                                     75 IVFGTTNGMTISTGLEYGPDNEANTGGQWVQDGGTANKTTVTSG--GLQ--RVNPGGSVS 130
                                                                                                                                                                                                                                                     363 DDGGTLDVRNGGTATTVSMGNGGVLLADSGAAVSGTRSDGKAFSIGGGQADALMLEKGSS 422
                                                                                                                         PTVHLNGIGSTL----TDTLLNTG------ATTNVTNDNVTDDEKKRAASVKDVLNA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 NLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSV 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            423 FILNAGDTAIDTIVNGGLFTARGGTLAGTTTLNNGAILTLSGKTVNNDTLTIREGDAL-L 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 511 QNLNNRIDNVDGNARAGIAQAIATAGLAQAYLPGKSMMAIGGGTYRGEA-----GYAIGY
                                                                                                                                                                                                                              GWNIKGVKPGTTASDNVDFVRT - - - - - - - YDTVEFLSADTKTTTVNVESKDNGKRTE
                                                                                                                                                                                                                                                                                                                           278 VKIG-AKTSVIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTAN
                                                                                                                                                                                                                                                                                                                                                                         25 RAEGTANTTVY------AGGDQTVHGHAL------DTTLNGGYQY---VHN
                                                                                                                                                                                                                                                                                                                                                                                                                             337 GQTGQADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 GGTAS----DTVVNSDGWQIVKNGGVAGNTTVNQKGRLQV--DAG-GTATNVTLKQ--GG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313 ALVISTAATVIGINRLGAFSVVEGKADNVV-----LENGGRLDVLIGHTAINIRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 SLGA-----GADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVA
                                                                                                                                                                          131 DTVISAGGGOSLOGRAVNTTLNGGEQWMHEGAIATGTVINDK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482 OGGSLTGNGSVEKSGSG 498
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P15320;
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                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                   FEMS Microbiol. Lett. 149:115-120(1997).
-i- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY FUNCTION AS AN ADHESIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.3%; Score 223; DB 1; Length 1039;
22.7%; Pred. No. 0.00047;
ve 64; Mismatches 255; Indels 158; Gaps
                                                                                                                      Henderson I.R., Meehan M., Owen P.; "Antigen 43, a phase-variable bipartite outer membrane protein, determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                              SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SL -> FF (IN STRAIN ML 308-225).
T -> K (IN STRAIN ML 308-225).
W -> L (IN STRAIN ML 308-225).
V -> F (IN STRAIN ML 308-225).
ATN -> STI (IN STRAIN ML 308-225).
A -> T (IN STRAIN ML 308-225).
B -> V (IN STRAIN ML 308-225).
E -> K (IN STRAIN ML 308-225).
E -> K (IN STRAIN ML 308-225).
G -> F (IN STRAIN ML 308-225).
G -> F (IN STRAIN ML 308-225).
G -> C (IN STRAIN ML 308-225).
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STRAIN ML 308-225).
STRAIN ML 308-225).
STRAIN ML 308-225).
                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.
SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTIGEN 43 ALPHA CHAIN.
ANTIGEN 43 BETA CHAIN.
K -> N (IN STRAIN ML 308-225)
SL -> FF (IN STRAIN ML 308-22
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STRAIN ML 308-225)
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5170D647C8DEEBE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000291; AAC75061.1; ALT_INIT.
EMBL; D90838; BAA15825.1; ALT_INIT.
EMBL; D90839; BAA15832.1; ALT_INIT.
EMBL; U3233, AAB41869.1; -.
ECOGENE; E32866; flu.
Outer membrane; Signal; Complete proteome.
in the genome of Escherichia coli K-12.";
Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N - 7 T (IN S)

S - 4 O (IN S)

S - 4 O (IN S)

H - 5 Y (IN S)

H - 5 Y (IN S)

GHL - 5 SHF (S)

S - 4 O (IN S)

A - 4 O (IN S)

A - 5 O (IN S)

C - 6 O (IN S)

C - 7 O (IN S
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O -> L (IN
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                                                                                                  MEDLINE=97257509; PubMed=9103983;
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61 039 AA;
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Matches 140;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Usage by and for commercial
                                                                                                                                                                                                                                                     MEDIINE-88257037; PubMed-3290200;
Poole K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                      CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 170:3177-3188(1988).
                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
PRT; 1608 AA.
                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
STANDARD;
                                                                                      Hemolysin precursor.
                                                                                                                            Serratia marcescens
                                                                                                                                                                              NCBI_TaxID=615;
                                                 01-APR-1990
01-NOV-1990
                                                                                                                                                                                                                                                                                                                 marcescens."
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61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120

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29

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-----TVNGG---TLANHDNQ 74

1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60 LNTCYRLVWNHMTGAFVVASELARARGKRGGVAVALSLAAVTSLPVLAA-----DIVVH 58

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 -LKAGDNLKIKQ-NTNENTNENTNDSSFTYSLKKDL-TDLTSVETEKLSFGANGNKVNIT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG----GFQRVNSGAVATGTVLSGGTQNVSSGGSAISTSVYNSGVQTVFAGATVTDTTVN 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGGNQNISSGGIVSETTVNVSGTQNIYSGGSALSANIKGSQIVNSEGTAINTLVSDGGYQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 HIRNGGIASGTIVNQSGYVNISSGGYAESTIINSGGTLRVLSDGYARGTILNNSGRENVS 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGGVSYNAMINTGGNQYIYSDGEATAAIVNTSGFQRINSG----GTAPVQNSVVVTRTVS 465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNKISRIIWNSALNAWVVVSELTRNH-----TKRASATVATA--VLATLLFATVQANA 51
                                                                                                                                 | | : : : | | | TISTIVNSGGIQRVSSGGVASATNLSGGAQNIYNLGHASNTVIFSGGNQTIFSGGITDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234 -VKPGTTASDNV------DFVRTYDTVEFLS-ADTKTTTVNVESKDN--
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                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEGTE----------------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.9%; Score 209; DB 1; Length 1286;
Best Local Similarity 18.3%; Pred. No. 0.003;
Matches 157; Conservative 111; Mismatches 287; Indels 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AUCOLL, The PIR; S28634; S28634; S28634. Cell adhesion; Signal; Outer membrane; Plasmid. The Against Alba-I.
                                                                                         AND SEQUENCE OF 50-56
                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Outer membrane.
                                                                                                       STRAIN=2787 (0126:H27);
MEDLINE=92326638; PubMed=1625582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -AKEVIDAVNKAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1286
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SEQUENCE FROM N.A.,
                                                            NCBI_TaxID=562;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| || : || || 331 ASSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGNKVSFLAADDKTASNTEQTKIGGGF 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TNVAQLKGVAQNLN------NRIDNVDGNARAGIAQAIATAGLAQAYL 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EG--TGEKEGTEDSNWAVYFDEKRVLKA-----GAITLKAGDNLKIKQNTNENTN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVSLGAGADAPTLSVDDEG-----ALNVGSKDANKPVRITN---VAPGVKEGDV---- 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543 PGKSMMAIGGGTYRGEAGYAIGYSSISDTGNW------VIKGTASGNSRGHFGTSA 592
                                                                                                                                                                                                                          RNHTKRASATVATAVLATLL----FATVQANATDDDDLYLE---PVQRTAVVLSFRSDK 75
                                                                                                                                                                                                                                                                                                  ---DSSFTYSLKKDLTDLTSVETEKLSFGANG---NKVNITSDTKGLNFAKETAGTNGDP
                                                                                                                                                                                                                                                                                                                                                                                                                         TVHLNG-IGSTLTDTLL--NTGATTNVTNDNVTDDEKKRAASVKDVLNA----GWNIKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 KPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKD-NGKRT----EVKIGAKTSVIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 GWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    847 VGGAYQENAAGVDHLAAADTASTTTTKTDVGVNI------GANVDYSAVTRPVER
                                                                                                                                                                                                                                                                                                                                                               -----TANGQTGQADKFETVTSGTKVTFASGNGTTA------
                                                                                                                                                               Score 211; DB 1; Length 1608;
Pred. No. 0.0031;
); Mismatches 275; Indels 196;
                                                                                                                                                             Length 1608;
                                                                                                       31 1608 HEMOLYSIN.
1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
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                        EMBL; M22618; AAA50323.1;
PIR; A28182; A28182.
Hemolysis; Toxin; Outer membrane; Signal.
SIGNAL
entities requires a license agreement (St
or send an email to license@isb-sib.ch).
                                                                                                                                                                                            89;
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Similarity 22.1%;
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                                                                                                                   SEQUENCE
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MEDLINE=94100243; PubMed=8274505;
Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
"An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and MOM38.":
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STRAIN=K1Z / MG1655;
MEDLINE=97426617; bubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
| : | | : | | : | SAAKPFDAEVYSGGKQTVYLWRGIWYSNFLTAVWSMFPGTASGANVNLSGRLNAFAGNVV
                                                                              GT-----KVTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQ--NSGWNLDSKA
                                                                                                                               403 VAGSSGKVI--SGNVSPSKGKMDETVNINAGN---NIEITRNGKNIDIATSMT-PQFSSV
                                                                                                                                                                     586 INEGGAQFVYDGGQVTGTNIKNGGTIRVDSGASALNIALS-SGGNLFTSTGATLPELTTM
                                                                                                                                                                                                                                                                                 477 VGSKDANKPVRITNVA-----PGVKEGDVTNVAQLKGV---AQNLNNRIDNVDG
                                                                                                                                                                                                                                              645 AALSVSQNHASNIVLENGGLLRVTSGGTATDTTVNSAGRLRIDDGGTINGTTTINADGIV
                                                                                                                                                                                                                                                                                                                                                            NARAGIAQAIATAGLA---QAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTG----NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDEK_ECOLI STANDARD; PRT; 1325 AA. P32051; P76140; P77168; Clord-1993 (Rel. 27, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical lipoprotein ydek precursor (ORFT) VDEK OR ORFT OR B1510.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48 ---TLGVLLALSGSASGASLEVDNDQITNIDTDVAYDAYLVGWYGTGVLNILAGGNASLT 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 TITTSVIGANEDSEGTVNVLGGTWRL------YDSGNNARPLNVGQSGTGTL 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 QNT-----NENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNI-TSDTKGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            336 HWNFLGTGEAFRYIYIGDAGDGELNVSSEGKVDSGIITAG----MKET----GTGNITVKDK
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                                                                                                                            CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
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N -> K (IN REF. 3).
M -> S (IN REF. 3).
MW; 26A3A066FA19AD7D CRC64;
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SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT
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EcoGene; EG11780; ydeK.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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EMBL; D90794; BAA15197.1; ALT_INIT.
EMBL; X73295; CAA51730.1; ALT_FRAME.
                                                                                                                                                                  FRAMESHIFT IN POSITION 653.
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      450 TIIGVAGVGNLNISDGG--KFVSQNITFLGDKASGIGTLNLMDATSSFDTVGINVGNF-G 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.; *A protective protein antigen of Rickettsia rickettsii has tandemly
                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Last Sequence update)
LoCY-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmpA).
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                                                                                                      507 SGIVNVSNGATLNSTGYGFIGGNASGKGIVNISTDSLMNLK-TSSTNAOLLOVGYLGT
                                                                545 KSMMAIGGGTYRGEAGYAI-----GYSSISDTGNWVIKGTASGNSR----GHFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeated, near-identical sequences.";
Infect. Immun. 58:2760.2759(1990).
-!- FUNCTION: ELICITS PROFECTIVE IMMUNTY.
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED S-LAVER WITH HEXAGONAL. SYMMETRY.
-!- PTM: GLYCOSYLATED (PROBABLE).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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OUTER MEMBRANE PROTEIN A.
13 X APPROXIMATE TANDEM REPEATS.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=783;
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A9D6646C089DF087 CRC64;
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Pfam; PF02708; rOmpA_rOmpB; 1.
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SEQUENCE FROM N.A.
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Gaps

6.5%; Score 199; DB 1; Length 2249; 22.3%; Pred. No. 0.018; Live 71; Mismatches 261; Indels 166;

Matches 143; Conservative

Similarity

Query Match Best Local

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436
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                                                                                                                                                                                                                                                      250 TLTNANAVLTGAIDNTTGGDNVGVLNLNGALSQVTGDIGNTNSLATISVGAGTATLGGAV 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370 VGAGLLQ---VQGGVVKANTINLTDNASAVTFT--NPVVVTGAIDNTGNANNGIVTFTGN 424
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"Nucleotide sequencing of the Proteus mirabilis calcium-independent
"Nucleotide sequencing of the Proteus mirabilis calcium-independent
"Nucleotide sequencing of the Proteus Sequence similarity with the
Serratia marcescens hemolysin genes (shiha and shib).";
J. Bacteriol. 172:1206-1216(1990).
-I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
  98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
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                                              ---GAI-----TLKAGDNLKIKQ
                                                                                                                                     NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANG------NKVNITS--DT
                                                                                                                                                            166 KGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNV---TDDEKKRAASVK
                                                                                                                                                                                                                                                                                                              DVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTT----TVNVESKD---NG--
                                                                                                                                                                                                                                                                                                                                                                                                        274 -KRTEVKIGAKTSVIKEKDGKLVTG----KGKGENGSSTDEGEGLVTAK----EVIDAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---VGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINA--GNNIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRNGKNIDIAT - - - - - - - - SMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
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Last annotation update)
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STRAIN-ISOLATE 477-12;
MEDLINE-90170827; Pubmed-2407716;
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01-AUG-1990 (Rel. 15, Last seq
01-NOV-1990 (Rel. 16, Last anno
                                                D----- EKRVLKA----
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P16466;
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576 IKGTASGNSRGHFGTSASVGY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
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SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 KLVTGKGKGENGSSTDE---GEGLVTAKEVIDAVNK---AGWRMKTT-----TANGQTG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              441 K-NIDIATSMTPQFSSVSLGAGADAPTL-SVDDEGALNVGSKDANKPVRITNVAPGVKEG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 AGTNGDPTVH-----LNGIGS-----TLTDTLLNTGATTNVTND-NVTDDEK 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 YLPGKSMMAIG-----SGTYRGEAGYAIGYSSI------SDTGNWV 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 TYS-----LKKDLT----DL----TSVETEKLSFGANGNKVNITSDTKGLNFAKET 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                925 VEVGIKGGGSQQSQTDSQAVSTSINAGKIDIDSNNKLHDQGTHYQSTQEGISLTANTHTS 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 TRNHTKRASATVATA-----VLATLLFATVQANATDDDDLYLEPVQRTAVVLSF 71
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HITHTTNKNTSTETEQANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            866 DVGVNLDYSGVTKPVKKAIEDGŸNT-TKPGNNTDLTKKVTARDAIANLANLSNLETPNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 GW--NLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITR------NG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    246;
                                                                                                                                                                                                                                                                                                                                                                                                            6.4%; Score 195; DB 1; Length 1577; 20.5%; Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 20.5%; Pred. No. 0.018;
Matches 152; Conservative 110; Mismatches 233; Indels
                                                                                                                                                                                                                                                                                                                                 HEMOLYSIN.
W; 175975E0C924B2D9 CRC64;
                                                                                                                                                                                                                                                                                             Hemolysis; Toxin; Outer membrane; Signal.
SUBCELLULAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                 30 1577 HEM
1577 AA; 165869 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        679 KTSLAITGHAKEVEDKQYSAGF----
                                                                                                                                                                                                                                                    EMBL; M30186; AAA25657.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makin T., Mizobuchi K., Mori H., Mori T., Moroura K., Makade S., Nakamura Y., Rashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takeuchi Y., Mada C., Yamamoto Y., Horiuchi T., and S70-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92190338; PubMed=1665988;
Moszer I., Glaser P., Danchin A.;
Multiple IS insertion sequences near the replication terminus in Escherichia coli K-12.;
Biochimie 73:1361-1374(1991).
-! SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-! CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID ISSD/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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-> V (IN REF. 2).
: B83A12C8B53220EE CRC64;
                                                                                       D1-FBB-1994 (Rel. 28, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein ydba.
FRAPA OR B1401/B1405.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12;
MEDLINE=97251357; PubMed=9097039;
1262 ITSAQSTDYKNNWGT--DIGF 1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 464-2003 FROM N.A.
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                                                                                                                                                                                                                                     Escherichia coli
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MEDLINE=94171067; PubMed=8125327;

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42;
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                                                                                                                                                                                                               143 NNDVILDKTEKTLTIRDSVFTYTENADGT---ISLQDSNGRKATINLWQI--DEANNTVA 197
                                                                                                                                                                                                                                                                                    96 -KRVLKAGAITLK-----AGDNLKIKQNTNENTNESFTYSLKKDLTDLTSV 145
                                                                                                                                                                                                                                                                                                                                                          198 LEGVSADGATKWQYNHNGELVITGDNATV--NNNGKTTVDGKDSTGT---EINGNNGKVI 252
                                                                                                                                                                                                                                                                                                                                                                                                                           ETEKLSFGANGNKVNITSDT----KG-----KG-----LNFAKETAGTNGD 180
                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 -EKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              373 VDNKGTMTVTDPESIGIOVDG-DOAVVNNEGESAITNGGTGTQINGDDATANNNGKTTVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 -EGALNVGSKDANKPVRIT-----NVA-----PGV-----KEGDVTNVAOLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           655 KATGINV-SGDAN-TVNITGNVLVDKDKDKTADNAAEYFFDPSVGINVYGSDNNVTLDGKLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  713 VVSDSEVTSROSNLFDGSAE-----KTSGL------VVIGDG-----
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                                                                            Indels 207;
          Length 2003;
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Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 PTVHLNG-----IGSTLTDTLLNTGATTNVTNDNVTDD------
          DB 1;
                                                                            Mismatches 232;
                                                                                                                                          DDDLYLEPVQRTAV - - - VLSFRSDKEGTGEKEGTEDSN - - -
   Score 190.5; Di
Pred. No. 0.04;
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6.3%; Scor
22.9%; Predictive 95; 1
                                                                            Conservative
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                                                                            Matches 159;
       Query Match
                                           Local
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AND MOROCCAN).
          Crocquet-Valdes P.A., Weiss K., Walker D.H.; "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain)."; Gene 140:115-119(1994).
                                                                                                                                                                                                                                                                                                            "Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rOmpA.";
J. Clin. Microbiol. 34:2058-2065(1996).
                                                                                                                                                                                        "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N -> H (IN STRAIN MOROCCAN).
M -> I (IN STRAIN INDIAN TICK TYPHUS).
Q -> K (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 953-2012 FROM N.A.
STRAIN=Indian tick typhus, MI, Malish 7, and Moroccan;
Raoult D., Fournier P.E., Roux V.;
"Phylogenetic analysis of spotted fever group rickettslae by study
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the outer surface protein rompa.";
submitted (DEC-1996) to the EMBLYGenBank/DDBJ databases.
-!- FUNCTION: ELICITE PROTECTIVE IMMUNITY (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED IS S-LAYER WITH HEXACONAL SYMMETRY.
-!- PIM: GLYCOSYLATED (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                            Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pram; PFU2/U8; rOmpA_rOmpB; 1.
Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
                                                                                                                                                                                                                                                           STRAIN=Indian tick typhus, MI, Malish 7, and Moroccan; MEDLINE=97015921; PubMed-8862558; Roux V., Fournier P.E., Raoult D.;
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                                                                                                           STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
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EMBL; AE008674; AAL03811.1; -.
EMBL; U43794; AAB49549.1; -.
EMBL; U43798; AAB49550.1; -.
EMBL; U45244; AAB49551.1; -.
EMBL; U46918; AAB4956.1; -.
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                                                                                                                                                                                                                                           SEQUENCE OF 8-204 FROM N.A.
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U83448; AAC35184.1;
U83453; AAC35189.1;
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
0uter membrane protein B precursor (168 KDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (TompB)
(Tomp B) [Contains: 120 KDa surface-exposed protein (Surface protein antigen) antigen) (120 KDa outer membrane protein ompB); 32 KDa beta peptidel.
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-i- FUNCTION: THE 120 kDa SURRACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-i- SUBCELLUIAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A LAYER WITH HEXAGONAL SYMMETRY.

-i- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                       -----VAPGVKEGDV-------TNVAQLKGVAQNLNNR
                                                                                                                                                                                                                                                                                                                                                                                              1055 SALVLSNLTGVGVNNILLAADLVAPGVDEGTVVFDGGVNGLNIGSNVA----GAARN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    517 IDNVDGNA-----RAGIAQAIATAGLAQAYLPGK----SMMAIGGGTYR-GEAGYAI
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Rickettsiaceae; Rickettsieae; Rickettsia.
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MEDLINE=92167802; PubMed=1724278;
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InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB: 1.
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encoding the

INFECTION

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Gilmore R.D. Jr., Joste N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encoding the state of the sequence analysis of the gene encoding the mol. Microbiol. 3:1579-1586(1989).

-i- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION. SUCCELL WALL. THIS BACTERIUM IS COVERED BY CLIANDE WITHEN HEAVACOUNT.
            MEDLINE=90136087; PubMed=2515418;
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                                                                                                                                                             241 GIIFNTDANNANTLNLQAGGT-TINFTGTDGTGRLVLLSKHAAATNFNITGSLGGNLKGV 299
                                                                           Gaps
                                                                                               ---LFATVQA-NATDDD 55
                                                                                                                                                                                                                                                                                     FGNLAAQIKVPNAITILTGNFTGDASNPGNTAG-----VITFDANGTLESASADANVAVTN
                                                                                                                                                                                                                                                                                                                               114 IKQNT-----NENTNENTND----SSFTYSLKKDLTDLTSVETEKLSFGANG
                                                                                                                                                                                                       300 IEFNTVAVDGQLTANAGAANAVIGTNNGAGRAAGFVVSVD------NG
                                                                                                                                                                                                                           NKVNITSDTKGLNFAKETAGTNGDPTV-HLNGIGSTLTDTLLNTGATTNVTNDN--VTDD
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                                                                          Indels 181;
                                                    Length 1654;
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Rickettsiaceae; Rickettsieae; Rickettsia.
                     D7AB70FB7087F618 CRC64;
                                                    Score 185.5; DB 1;
Pred. No. 0.056;
81; Mismatches 272;
  KDA BETA PEPTIDE
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Last annotation update)
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                                                                                              AWVVVSELTRNHTKRA-----SATVATAVLATL--
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18; Conservative
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01-FEB-1996
01-MAR-2002
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P14914;
                                                                         Matches 158;
                     SEQUENCE
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Best Local (
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120K_RICRI
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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S-LAYER WITH HEXAGONAL SYMMETRY.
-!- MISCELLANEOUS: ITS C-TERMINGS POTENTIALLY MAY BEAR THE EPITOPES CONFERRING ANTIGENICITY FOU THE PROTEIN.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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21.9%; Pred. No. 0.045;
Live 91; Mismatches 269; Indels 218;
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InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
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Matches 162; Conservative
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                        246
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           201
                        |: ||: ||: || || || ||: || || SI--FKLADGTVING-KVNQTA------LVGGALAAGTITLDG-SATITGDIGNAGG 178
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                                                                                                                                                                                                                                                   --SGTKVTF---ASGNGTTATVSKDD---QGNITVKYDVNVGDALNVNQLQNSG---WNL 398
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                                                                                                                                                                                                     --EGEGLVTAKEVIDAVNKAGWRMKTTTAN---------GQTG--QADKFETVT
            SVETEKLSFGA - - NGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNTGA
                                                                                AAALQRITLANDAK-----KTLTLGGANIIGAGGGTIDLQANGGTIKLTSTQNNIVVDF
                                                                                                         -----VEFLSADTKT-----TTVNVESKDNGKRTE
                                                                                                                               233 DLAIATDQTGVVDASSLTNAQTLTINGKIGTIGANNKTLGQFNIGSSKTVLSNGNVAINE
                                                                                                                                                       VKIGAKTSVIKEKDGKLVT-----GKGK-------GEN-GSSTD-----
                                                                                                                                                                                                                                                                                                                       472 NKQAAPVNALKQITVSGPGNVVINEIGNAGNHHGAVTDTIAFENSSLGAVVFLPRGIPFN
                                                                                                                                                                                                                                                                                                                                                ---POFSSVSLGAGAD----
                                                        TINVINDNVTDDEKKRAASVKDVLNAGWNIKGVKPGT------TASDN---VDF
                                                                                                                                                                                                                                                                                                  399 DSKA-----VAGSSGKVIS--GNVSPSKGKMDETVNI-------VAGSSGKVIS--GNVSPSKGKMDETVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BIGA_SALTY STANDARD; PRT; 1953 AA.

B15927; P25928; O9XCQ3;
01-MAY-1992 (Rel. 2, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
putative surface-exposed virulence protein bigA precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stoilljkovic I., Valentine P., Heffron F.; "Salmonella typhimurium rhs homolog."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                NAGNNIEIT-----RNGKNIDIATSMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      702 MIGTTKANN----GTVTYLG 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 IKGTASGNSRGHFGTSASVG 595
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SEQUENCE FROM N.A.
                                                                                                         ---VRTYDT---
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NCBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIGA OR STM3478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28;
                                                                                                                                                                                                                                             cofactor.";
J. Bacteriol. 173:325-333(1991).
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 414 and 732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NENTNDSSFTYSLKKDLT--DLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 QRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNENT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                       Wu J.Y., Siegel L.M., Kredich N.M.; "High-level expression of Escherichia coli NADPH-sulfite reductase: requirement for a cloned cysG plasmid to overcome limiting siroheme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 IWNSAL--NAWVVVSELTRNHTKRASAT---VATAVLATLLFATVQANATDDDDLYLEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete proteome.
POTENTIAL.
PUTATIVE SURFACE-EXPOSED VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.072;
ches 275; Indels 184;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REF. 1).
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SA -> T (IN REF. 1).
W; 611B3F1C954D91AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN BIGA.
15 X 11 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRGDDDVTPPDD (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 (INCOMPLETE).
D -> DRGDDDVTPPDD (
A -> R (IN REF. 3).
D -> N (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.1%; Score 185; DB 20.6%; Pred. No. 0.07: tive 91; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AF133696; AAD39458.1; -.
EMBL, AE008859; AAL22340.1; -.
EMBL, A46066; AAA2704.1; ALT_FRAME.
EMBL; M64606; AAA27043.1; ALT_FRAME.
                                                                                                                                    STRAIN=LT2;
MEDLINE=91100301; PubMed=1987123;
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1 27
28 1953
                                                                                                               SEQUENCE OF 1-765 FROM N.A.
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Matches 143; Conservative
                                                                   Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG10437; bigA.
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177
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PIR; D39200; D39200.
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1953
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Virulence; F
SIGNAL
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CONFLICT
SEQUENCE
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SEQUENCE OF 353-1655 FROM N.A.

STRAIN-Malish

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OMFB_RICCN GyC45;

16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
(Surface protein a Protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                     367
                                                                                                                                                                                                                                                                                                                                                                                                      -GDMSQVTLDGDINV --- VSVQDSEGVFSSATGVSVSGDSNAVDITGNVNISADYGQDDL 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                   473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 474 ALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIA 533
NTLTGDSSVTDGATGMVISGDGTTNTISGHSTVDNATGALISGNGTTTNFAGDIAVSGGG 440
                                      PTVHLNGIGSTLTDT----LLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP 236
                                                                                                                                                             ------ DNAGSTTVSGADATALYIEGDNALVI 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB)."; Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fournier P.-E., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           807 RVNNGGSLILGDDSVVDVNVSYIPTGYYTYNALLMADGEGTSIENKGDITSHGVYSVIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TAGLAQAYLP-----GKSMMAIGGGTYRGEAG-----YAI---
                                                                            TAIIIDGDNATIKNTGTSDISGAGSTGTVIDGNNARVNNDGDMTITD------GGTG
                                                                                                                    GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                                                                                                           528 NEGNOTISGGAVGTRIDGDDAHTTNTGDIAVDGAGSAAVIINGDNGSLTQAGDLLVTDGA
                                                                                                                                                                                                                                                                                 317 KEVI--DAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTF-----ASGNGTTATVS
                                                                                                                                                                                                                                                                                                                          588 MGIITYGTGNEA----KNTGNATVRDADSVGFVVAGEKNTFKNKGDIDVSLNGTGALVS
                                                                                                                                                                                                                                                                                                                                                                                                                                              419 -KGKMDETVNINAGNNIEITRNGK-NI---DIATSMTPQFSSVSLGAGADAPTLSVDDEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757 GINI -- THSEDPLDGTS-----ADITGISVSGNSTVTLNGH-STIDTNTVVGGHVVLA
                                                                                                                                                                                                                                                                                                                                                                    368 KDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKV-ISGNVSPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barb
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 -GYSSISDTGNWVIKGTASGNSRGHFGTSASVG 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Indian tick typhus, and Malish 7; MEDLINE-20393643; PubMed-10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21442074; PubMed=11557893;
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                                                                                                                                                          GHITGDNVVI
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STRAIN=Malish 7;
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                                                                                                                                                                                                     GKG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raoult D.;
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381
                                      181
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                                                                                                                                                                                                                                                                                                                                                between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                Stenos J., Walker D.;
Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia
australis, the most divergent rickettsia of the spotted fever group.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
6 -> 5 (IN STRAIN INDIAN TICK TYPHUS).
7 X (IN STRAIN INDIAN TICK TYPHUS).
8 Y >> A (IN STRAIN INDIAN TICK TYPHUS).
9 Y -> A (IN STRAIN INDIAN TICK TYPHUS).
1 Y (IN STRAIN INDIAN TICK TYPHUS).
2 X -> L (IN STRAIN INDIAN TICK TYPHUS).
4 Y (IN REF. 3).
5 Y (IN REF. 3).
6 Y S (IN REF. 3).
6 Y S (IN REF. 3).
7 Y (IN REF. 3).
7 Y (IN REF. 3).
8 Y S (IN REF. 3).
9 Y S (IN REF. 3).
1 Y S (IN REF. 3).
1 Y S (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 SFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLK------IKQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 TF-----NGTDGTGRLVLLSKNAAATDFNVTGSLGGNLKGIIEFNTVAVNGQLKA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 NAGANAAVIGTNNGAGRAAGFVVSVD-------NGKVATIDGQVYAKDM 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 TLNGNFTGDASNPGNTAG----VITFDANGTLASASADANVAVTNNITAIEASGAGVVQ 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 NGTLN-----VTNGFIKVSSKSFATVNVINIGDGQGIMFNTDADNVNTLNLQANGATI 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 AKETAGTNGDPT----VHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKD--- 223
                                                                                                                                                                                               -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 NSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLEPVQRTAVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 NINEN-----INENTNDSS-FTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 VLNAGWNIKGVKPGTTASDNVDFVRTYD---TVEFLSADTKTTTVN----VESKDNG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 356 VIQSANAVGQVNFRHIVDVGTDGTTAFKTAASKVAITQNSNFGTTDFGNLAAQIIVPNTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1655;
                                                                                                                                                                                                                                                                  LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.1%; Score 184.5; DB 1;
22.1%; Pred. No. 0.063;
ive 76; Mismatches 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF149110; AAD39533.1; -.
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE008659; AAL03623.1; -. EMBL; AF123721; AAF34124.1; -. EMBL; AF123726; AAF34129.1; -.
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Best Local Similarity 22.18
Matches 147; Conservative
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413
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                                                                                                                                                                                                                        424
                                                                                                                                                                                                                                                                                                                                                                                    641 DVAINELVIGNNGAVQFAHNTYLITRTINAAGOGKIIFNPVVNNNTTLATGTNLGS-ATN 699
                                                                                                                                                                                                                                                                                                                                                                                                                                          471 DEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDG-NARAGIA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TVGGQQGNKFNTVALDNGTTVKFLGNATFIAAN-STLQIGGNYTADFVASA 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRYSTALLIZATION IN SUPERCOLED WATER.
SUBCELULAR LOCATION IN SUPERCOLED WATER.
SUBCELULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS 153 IMPERECT REPEATS OF THE CONSENSUS
CCTAPEPTIDE A-G-Y-G-Y-T-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
NISCELARBOUS: A STRUCTHAR MODEL IS SUGGESTED IN WHICH THE ICE
NUCLEATION PROTEIN DISPLAYS A SYMMERRY RELATED TO THAT OF ICE.
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                            ----GKGENGSSTDEGEGLVTAKEVID
                                                                                                             AVNKAGWRMKTTTANGQTGQADKFETVT - - - - - - SGTKVTFASGNGTTATVSKDDQG
                                                                                                                                                                                                                                                                                                                                   TVNIN---AGNN--IEITRNGKNIDIATSMTPQ----FSSV----SLGAGADAPTLSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAIATAGLAQ-----AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASG
                                                                                                                                                                                                                        NITVKYDV-----NVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).
-1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Conserved repetition in the ice nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
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----KRTEVKIGAKTSVIKEKDGKLVTGK----
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01-NOV-1990
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1058 GTAGADSTLIAGYGSTQTAGSDSSLTAGYGST-----TAGYGSTGT-AG 1109
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MEDLINE-94150718; PubMed=7906398;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Molfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                              132 TYSLKKDLT----DLTSVETEKLSFGA------NGNKVNITSDTKGLNFAKE 173
                                                                                                                                                                                                                                                                                                        77 GTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN----ENTNENTNDSSF 131
                                                                                                                                                                                                                                                                                                                                                     735 GSTQTSGSDSSLTAGYGSTQTARKGSDVTAGYGSTGTAGADSTLIAGYGSTQTSGSDSSL 794
                                                                                                                                                                                                                                                     Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222 KDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 AKTSVIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 795 TAGYGSTQTARKGSDITAGYGSTGTAGADSTLIAGYGSTQTSGSDSSLIAGYGSTQTARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TAGTNGDPTVHLNGIGSTLT----DTLLNTGATTNVTNDNVTDDEKKRAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 ADKFETVTSGTKVTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              402 AVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         462 ADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            855 GSDVTAGYGSTGTAGADSTLISGYGSTQTAGSDSSLTAGYGSTQTARKGSD-----
                                                                                                                                                                                                                                                98;
                                                                                                                                                                                                Length 1567;
                                                                                                                                                                                       6.0%; Score 182; DB 1; Length 150
20.2%; Pred. No. 0.079;
ive 83; Mismatches 274; Indels
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01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 96.6 kDa protein F59B2.12 in chromosome III.
F59B2.12.
                                                                               nucleation; Repeat; Outer membrane.
JENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
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Pfam; PF00818; Ice_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
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Best Local Similarity 20.2°
Matches 115; Conservative
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1645 AA

PRT;

STANDARD;

OMPB\_RICTY

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Latraile P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R., Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Sulston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Waterston R., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      347 TVTSGTKVTFASG------NG--TTATVSKDDQ------GNITVKYDVNVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :|| : :: || :|: || :| SLNESSIE-SGRKAESRNTAADTLDSVDANGTVSSSHSKSASGTSLDENHNKTHALQAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RITHVAPGVKEGDVTHVAQLKGVAQNLHNRIDHVDGNARAGIAQAIATAGLAQAYLPGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ASD-----AHSNFESLDAQG-----NKKSQNYSKKAASASGSNADFESNLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193 NADGTFLRNNTGHKNTDEHLSHNVLDENAQMSIGADGTSHNITNRKGSVGDSHNA----
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                                                                                                                                            '2.2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 MMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGYQW 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 181; DB 1; Length 918;
Pred. No. 0.047;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.04
89; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 918 AA; 96560 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.0°
Best Local Similarity 21.8°
Matches 129; Conservative
                                                                                                                                                                                     Nature 368:32-38(1994).
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RESULT 15 OMPB\_RICTY

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hackstadt T. Messer R., Cleavage of the 120-kilodalton outer membrane protein of Tickettsiae: identification of an avirulent mutant deficient in processing."

Infect. Immun. 60:159-165(1992).

-! FUNCTION: THE 120 kDa SURRACE EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-! FUNCTION: THE 32 kDa BETA PEPTIDE NAY SERVE AS A MEMBRANE ANCHOR.

-! FUNCTION: THE 32 kDa BETA PEPTIDE NAY SERVE AS A MEMBRANE ANCHOR.

-! SUNCTION: THE 32 KDA BETA PEPTIDE NAY SERVE AS A MEMBRANE ANCHOR.

-! SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAXER WITH HEXAGONAL SYMMETRY.
                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                        MEDLINE=94040787; PubMed=8224886; Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.; Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.; "Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi."; Gene 133:129-133(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody binding sites on CNBr fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 KDA SURFACE-EXPOSED PROTEIN. 32 KDA BETA PEPTIDE.
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                                                                                                                                                                                                      Bacteria, Proteobacteria, alpha subdivision, Rickettsiales;
Rickettsiaceae, Rickettsieae, Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMBRANE ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H -> N (IN REF. 2).
V -> I (IN REF. 2).
G -> A (IN REF. 2).
G -> S (IN REF. 2).
WW: OCB5641C7EB185EE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-WILMINGTON;
MEDLINE-92114896; PubMed-1370573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION OF CLEAVAGE SITE. MEDLINE=92104668; PubMed=1729180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro; IPR003858; rOmpA_rOmpB.
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Matches 156; Conservative
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                                                                                                                                                                                     Rickettsia typhi.
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65 69 119	113	224	274	310	356 393	407	447	495 559	520 619	564 679	
KRASATVATAVLATLLFAPUQRNATDDDDLYLEPUQRT	SVITANSNNAITFNTPNG-NLNSLFLDTANTLAYTINENTLGFV ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGAN-GNKVNITSDTKGLN	FAKETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDV		RTEVKIGAKISVIKEKDGKLVTGKGKGENGSSTDEGBTDEGBTDEGBTDEGBTDEG	311EGLUTAKEVIDAVNKAGMRMKTTTANGQTGQADKFETVTSGTKUTF	ASGNGTTATVSKDDQGNITVKXDVNVGDALNVNQLQNSGWNLDSKAVAGSS :   :	GKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIAT   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   ::   :	SMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGV:	496 KEGLUNRIDNV	521 DGNARAGIAQAIATAGLAQAYLPGKSMMAIGGGTYRGEAGYAIG   :	565 YSSISDTGNWVIKGTASGNSRGHFGTSASVG 595 : :  :      :: 680 AADPINTDTALADGTNLGSAESPLSNIHFATKAANG 715
28 10 66	70	170	225	275	311	357 394	408	448	496	521 620	565
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Search completed: July 3, 2002, 08:48:58 Job time: 704 sec

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; Search time 100.13 Seconds
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1033.167 Million cell updates/sec
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1 MNKISRIIWNSALNAWVVVS......TASGNSRGHFGTSASVGYQW 598
                      Compugen Ltd
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GenCore version 4.5
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091955 neisseria m 091989 neisseria m 091972 neisseria m 091970 neisseria m 091971 neisseria m 091974 neisseria m 091984 neisseria m 091984 neisseria m 091981 neisseria m 091806 neisseria m 091806 pasteurella 091806 vylella fas 091808 salmonella 092604 vylella fas 091808 salmonella 09267 rhizobium m 098192 rhizobium m 091807 avylella fas 091808 serencella 091808 serencella 091808 avylella fas 091808 serencella 091618 serencella

09JPS5 09JPS9 09JPS9 09JPH0 09JQN1 09JQN1 09JPS1 09JPS1 09JPS1 09FS2D8 09FS2D8 09FS2D8 09FS2D8 09FS2D8 09FS2D8 09FS3C9 09FS3C9

5591 5600

2705.5 2702 2702 2686 2686 2637.5 2617.5 2617.5 2617.5 2617.5 2617.5 383.6 383.6 263.5 263

sp\_invertebrate:\*
sp\_mammal:\*
sp\_mhc:\*
sp\_organelle:\* sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_rvirus:\*
sp\_bacteriap:\* sp\_archea:\*
sp\_bacteria:\*
sp\_fungi:\*
sp\_human:\* sp\_archeap:\* sp\_plant:\* sp\_rodent:\* sp\_phage:\* SPTREMBL 19:\* Database

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

598 AA

PRT;

PRELIMINARY;

0930Y5

RESULT **0930Y5** 

ALIGNMENTS

09F285 054356 09L6T8 048031 09AL50

Q9RNI2 Q9L6T7

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## 091940 mersseria m 091pr0 netsseria m 091pr0 netsseria m 091pr2 netsseria m 091pr2 netsseria m 093qy4 netsseria m 091pr8 netsseria m 091pr8 netsseria m 091pr7 netsseria m 091pr7 netsseria m 091pr7 netsseria m 091pr7 netsseria m Q93qy5 neisseria Description 0930Y5 09JPT0 09JPS0 09JPR9 09JPP3 09JPR3 09JPR8 09JPR8 09JPR8 09JPR8 DB Length Query Match 9999.8 9999.8 9911.1 9911.1 999.3 899.3 3021 2982 2982 2982 2882 2852 2821.5 2772 2752.5 2752.5 2752.5 2765 2716.5 Score Result Š.

			0;			
Ol-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-DEC-2001 (TrEMBLRel. 19, Last annotation update) MHA OUTER MEMBRANE PROTEIN.	nun. Velisseria meningitidis. Sacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. NCBI_TaxID-487; [1]	SEQUENCE FROM N.A.  PROBLIN-B310;  PROBLE FROM N.A.  PROBLE I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  PROBLE I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  PROBLET OF A REPORTATION OF A gene encoding a novel outer membrane protein of Neisseria meningitidis.";  Submitted (JUN-1999) to the EMBL/GenBank/DD5J databases.  EMBL; AF157603; AAK68864.1; 18CEFFE6410A15DF CRC64;	ry Match 100.0%; Score 3042; DB 2; Length 598; Local Similarity 100.0%; Pred. No. 2e-118; ches 598; Conservative 0; Mismatches 0; Indels 0; Gaps	1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60	61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITIKAGDNIKIKQNTNE 120 	121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 180
	(TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19, MEMBRANE PROTEIN.	Lrel. 19, Lrel. 19, Lrel. 19, E PROTEIN. idis. cteria; be	11-DEC-2001 (TERMELTEL. 19, Created) 11-DEC-2001 (TERMELTEL. 19, Last sequence update) 11-DEC-2001 (TERMELTEL. 19, Last sequence update) 11-DEC-2001 (TERMELTEL. 19, Last annotation update) 11-DEC-2001 (TERMELTEL. 19, Last annotation update) 11-DEC-2001 (TERMELTEL. 19, Last annotation update) 14-DEC-2001 (TERMELTEL. 19, Last annotation, Neisseriaceae; Neisseria. 14-DEC-2001 (TERMELTEL. 19, Last Last Section Neisseriaceae; Neisseria. 15-DEC-2001 (TERMELTEL. 19, Last Last Section Neisseriaceae; Neis	01-DEC-2001 (TERMBLEAL 19, Created) 01-DEC-2001 (TERMBLEAL 19, Last sequence update) 01-DEC-2001 (TERMBLEAL 19, Last annotation update) NHHA OUTER MEMBRANE PROTEIN. NHHA. Nelsseria meningitidis. Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria. NCBI_TAXID=487; [1] SEQUENCE FROM N.A. STRAIN=BZ10; Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.; Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.; STRAIN=BZ10; Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.; SEQUENCE FOR N.A. SEQUENCE 508 N.P.; SUBMILIGIATION and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64; SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64; Best Local Similarity 100.0%; Score 3042; DB 2; Length 598; Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	rel. 19, Created) rel. 19, Last sequence update) rel. 19, Last sequence update) rel. 19, Last sequence update)  PROFEIN. clast annotation update)  a Y., Dieckelman M., Moxon R., Jennings M.P.; characterization of a gene encoding a novel outer lesseria meningitidis.*; lot the EMEL/GenBank/DDBJ databases. 62687 MW; 18CEFFE6410A15DF CRC64; 100.0%; Score 3042; DB 2; Length 598; 100.0%; Score 3042; DB 2; Length 598; ative 0; Mismatches 0; Indels 0; Gaps AWWVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60	rel. 19, Created)  rel. 19, Last annotation update)  rel. 19, Last sequence update)  rel. 19, Last annotation update)  PROTEIN.  teria; beta subdivision; Neisseriaceae; Neisseria.  teria; beta subdivision; Neisseriaceae; Neisseria.  teria; beta subdivision; Neisseriaceae; Neisseria.  to haracterization of a gene encoding a novel outer  Neisseria meningitidis.";  Neisseria meningitidis.";  Neisseria meningitidis.";  100.0%; Score 3042; DB 2; Length 598;  100.0%; Score 3042; DB 2; Length 598;  100.0%; Score 3042; DB 2; Length 598;  1101.0%; Drad. No. 2e-118;  111

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Q9JPR7 Q9JPS7 Q9JR18 Q9AQF0

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Best Local Similarity 99.3
Matches 594; Conservative
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                                                SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGK
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
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Pred. No. 3.6e-118;
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Science 287:1816-1820(2000).
EMBL; AF226359; AAF42508.1; -.
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Matches 597; Conservative
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.; "Identification and characterization of a gene encoding a novel outer membrane protein of Nelsseria meningitidis."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF226881; AAF42530.1; BMBL, AF26881; AAF4550.1; BMBL, AF157607, AK68868.1. SEQUENCE 598 AA.
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NCBL_TaxID=487;
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241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGK
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
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Pred. No. 1.5e-117;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation).
01-DEC-2001 (TrEMBLrel.)
01-DE
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                                                   1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
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STRAIN-BZ198, AND 297-0;
MEDLINE-20175756; PubMed-10710308;
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                                                                                                                                                                                                              NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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Pred. No. 6.1e-116;
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MEDLINE-20175756; PubMed-10710308;
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62718 MW;
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SEQUENCE FROM N.A.
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01-MAR-2001
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Q9JPR9 **09JPR9**;

RESULT Q9JPR9 GNA992

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NCBI_TaxID=487;
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Best Local Si
Matches 570)
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Q9JPI3;
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                                                                                                                                                                                                                                                                                        1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLXLE
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                                                                                                                                                                                                                               4:
"Identification and characterization of a gene encoding a membrane protein of Neisseria meningitidis.";
Submitted (JUN1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226368; AAF42517.1;
EMBL; AF226358; AAF42507.1;
EMBL; AF157604; AAF6865.1;
EMBL; AF157604; AAF6865.1;
SEQUENCE 594 AA; 62361 MW; 436BDDED68263C5C CRC64;
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on update)
                                                                                                                                                                                Score 2948; DB 2;
Pred. No. 1.5e-114;
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0UTER MEMBRANE PROTEIN GNA992.
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ni E., Zuo P.,
Tettelin H.,
                                                                                                                                                                                                                                                                                                              177 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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                  Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter Woxon E.R., Grandi G., Rappuoli R.; "Identification of Vaccine Candidates Against Serogroup B
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В
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STRAIN-MANG3/88, AND BA232;
MEDLINE-20176; PubWed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Aricoʻ
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1-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN (GNA992.
                                                                                                                                                                                                                                    Score 2882; DB 2;
Pred. No. 8.1e-112;
6; Mismatches 18;
                                                                                                                                                                             62114 MW; 1E2A63A78F53D256
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Bacteria, Proteobacteria, beta
                                                                                                                                                                                                                                    / Match 94.7%;
Local Similarity 95.3%;
les 570; Conservative
                                                                                                                                                       EMBL; AF226379; AAF42528.1;
SEQUENCE 594 AA; 62114 M
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P., "Identification and characterization of a gene encoding a novel a membrane protein of Neisseria meningitidis."; submitted (JUN-1999) to the EMBL, GenBank/DDBJ databases. EMBL, AF157605; AAK68866.1; - SEQUENCE 594 AA, 68297 MW; 9DDD48B04B3ABEA2 CRC64:
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Q9JPR8;
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Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti R., Marchtti E., Mora M., Nuti S Ratti G., Santini L., Savinio S., Scarselli M., Storni E., Zuo P., Hooder M., Hudt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.K., Granoff G., Rappuoli R.;

"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";

EMBL, AF226376; AAF42525.1; -.

EMBL, AF226369; AAF42518.1; -.
                                                                                                                                                                                                                                                                                                      PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE
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Last sequence update)
Last annotation update)
                                                                                                                                                        Score 2878; DB 2;
Pred. No. 1.2e-111;
; Mismatches 19;
                                                                                                                        62086 MW; 1B25E03B90D04B46
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                                                                                                                                                                     Similarity
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SEQUENCE FROM N.A.
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Best Local Simil
Matches 569; C
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Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.
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                                                                          PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE
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                              Indels
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE FAISSETIA MELSSETIA MENDITIGIA.
Score 2852; DB 2;
Pred. No. 1.4e-110;
5; Mismatches 23;
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 93.8%;
llarity 94.6%;
Conservative
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Query Match
Best Local Similarity
Matches 566; Conserv
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Neisseria

Neisseriaceae;

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414 NVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEG 473
                                                                                                                         Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Mood D.W., Jeffries A.C., Sandeers N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; "Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFAT-----VQANATD
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                                                                                                                                                                                                                                                                                                                                62762 MW; 36256963E0598CD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 91.1%; Score 2772; DB 2; 91.4%; Pred. No. 2.8e-107;
                  Proteobacteria; beta subdivision;
                                                                                                                                                                                                                                                                            Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
                                                                                           STRAIN=E26; MEDLINE=20175756; PubMed=10710308;
                                                                                                                                                                                                                                                                                                                AF226371; AAF42520.1;
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Best Local Similarity 91.43
Matches 553; Conservative
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     Neisseria meningitidis
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                                       NCBI_TaxID=487;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ENTNENTINDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVK1GAKTSV1KEKDGKLVTGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASG
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Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., M. Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; Tidentlification of Vaccine Candidtes Against Serogroup B Meningococus by Whole-Genome Sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
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                                                                                                                                                                                    Jennings M.P.;
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                                                                                                                                                                                                                                                                                                                                                 599;
                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                             PraxIN=H38;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jenning "Identification and characterization of a gene encoding a membrane protein of Neisseria meningitidis.";
Submitted (JUN 1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1226383; AAF42532.1;
EMBL; AF157608; AAK68869.1;
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                                                                                                                                                                                                                                                                                             BBA16EBF53C1970C CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                               Query Match 92.8%; Score 2821.5; DB 2; Best Local Similarity 92.7%; Pred. No. 2.5e-109; Matches 555; Conservative 13; Mismatches 30; I
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Length 600;

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PRELIMINARY;
                                                                                    Neisseria meningitidis
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                                                                                                                            SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=487;
                                                                                              Bacteria;
                                                                                                                                                                                                                                                                   EMBL; AF2
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                        EPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQNT 118
                                                            Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                               1 MNKISRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLY-L
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                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                       Length 590;
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                                                                                                                                                                                                                                                      590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;
         01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0UTER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                    Score 2769; DB 2;
Pred. No. 3.7e-107;
9; Mismatches 25;
                                                                                                                                                                                                                        Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
                                                                                                                          MEDLINE=20175756; PubMed=10710308;
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 92.3%;
Matches 554; Conservative
                                                                                                                                                                                                                                           EMBL; AF226378; AAF42527
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                 STRAIN-NGE28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hudt E., Knapp B., Blair E., Mason T., Tettelin H., Mocon E.R., Grandi G., Rappuoli R.; Grandi G., Rappuoli R.; "Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ENTNENTINDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62693 MW; 46C2E974AF7F78E9 CRC64;
                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
00TER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.5%; Score 2752.5; DB 2 91.7%; Pred. No. 1.8e-106;
  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14; Mismatches
  599
PRT;
                                                                                                                                                                                                                                                                                    STRAIN=A22;
MEDLINE=20175756; PubMed=10710308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.79
Matches 551; Conservative
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Mon Jul

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Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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EMBL; AR226566; AAR42515.1. -
EEMBL; AR226566; AAR42515.1. -
                                1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVETAVLATLLFATVQASANNEEQEEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 SKDANKPVRITHVVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTF
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                       591
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                                                                                                                                                                                                                                                                                                                                                            STRAIN=BZ147;
MEDLINE=20175756; PubMed=10710308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 90.7:6; Conservative
                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=487;
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01-OCT-2000 (
01-DEC-2001 (
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Best Local Simi
Matches 546;
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                                                                                                                                                                                                                                                        Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
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                                                                                                                                                                                                                                                                                                                                                       Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Ratti G.L., Luzzi E., Maneti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hoxon D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., "Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPS
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                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AF226385; AAF42534.1;
SEQUENCE 598 AA; 62431 MW; 0881CC094F331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Mismatches
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(TrEMBLrel. 16, I
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Matches 545;
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STRAIN=MC58 / SEROGROUP B;

STRAIN=MC58 / SEROGROUP B;

STRAIN=MC58 / SEROGROUP B;

BELLIAR=-2017575; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Felsischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Nelsseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226375; AAF42524.1;
EMBL; AF226375; AAF42551.1;
EMBL; AF226377, AAF42516.1;
EMBL; AF226374; AAF42519.1;
EMBL; AF226374; AAF42519.1;
EMBL; AF157611; AAK68872.1;
                            596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis, and
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-MICS BY SERGOROUP B, BZ169, BZ83, AND H44/76;
STRAIN-MICS B, SERGOROUP B, BZ169, BZ83, AND H44/76;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                                                                     537 LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
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Length 591;
                                            Indels
  DB 16;
                       Pred. No. 5.4e-105;
89.3%; Score 2716.5; 90.7%; Pred. No. 5.4e
                                            13; Mismatches
                                            Matches 546; Conservative
                       Best Local Similarity
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 3, 2002, 08:36:23 ; Search time 104.77 Seconds (without alignments) 629.740 Million cell updates/sec

Run on:

Title:

US-09-771-382-9 Perfect score:

3023 1 MNKIYRIIWNSALNAWVVVS.....TASGNSRGHFGASASVGYQW 594 **BLOSUM62** Scoring table: Sequence:

Gapop 10.0 , Gapext 0.5

747574 seqs, 111073796 residues Searched:

747574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_032802:\* Database :

1. \SIDSI\gcgdata\hold \geneseq\geneseq\embl\AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

_	Description	A surface protein	N. meningitidis BZ	A surface protein	N. meningitidis H1	A surface protein	N. meningitidis BZ	A surface protein	BASB029 amino acid	N. meningitidis EG	A surface protein	N. meningitidis H3
	ID		AAU06179	AAY23742	AAU06177	AAY23738	AAU06178	AAY23740	AAY57044	AAU06174	AAY23743	AAU06176
	DB	20	22	20	22	20	22	20	21	22	20	22
	Length	594	594	598	598	598	298	594	594	594	599	599
ا عو	e Match Length DB I	100.0	100.0	98.3	98.3	97.5	97.5	95.1	95.1	95.1	92.7	92.7
	Score	3023	3023	2971	2971	2948	2948	2874	2874	2874	2802.5	2802.5
+100	NO.	-	7	m	4	S	9	7	œ	6	10	11

Neisseria meningitidis surface proteins useful for treating N. meningitidis infections

## ALIGNMENTS

Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide. A surface protein of Neisseria meningitidis. AAY23739 standard; Protein; 594 AA. Peak IRA; 98WO-AU01031. 97GB-0026398. (ISIS-) ISIS INNOVATION LTD. (UYQU) UNIV QUEENSLAND. (first entry) Jennings MP, Moxon ER, Neisseria meningitidis. WPI; 1999-418754/35. N-PSDB; AAX85791. WO9931132-A1. 14-DEC-1998; 12-DEC-1997; 08-SEP-1999 24-JUN-1999 AAY23739; AAY23739 RESULT 

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Location/Qualifiers

/label= C1

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                                                                                                                                                                                         PVRITHVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
               The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                 100.0%; Score 3023; DB 20;
100.0%; Pred. No. 4.3e-175;
tive 0; Mismatches 0;
Claim 1; Page 95-97; 132pp; English.
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Best Local 9
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA chofofi82-AM06186; The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylatcic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA (from N. meningitidis strain BZ198 is 1 of 10 NhhA polypeptide sequences (AMU06171-AMU06180) from 10 different N. meningitidis strains given in the present invention.
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/note= "Conserved region 2"
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Matches 594; Conservative
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N. meningitidis B2198 surface antigen NhhA polypeptide sequence. Surface antigen NhhA; meningococcal disease; meningitis vaccine

Neisseria meningitidis strain BZ198

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                                                                   The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                                                                                                                                                                                                                                                  Length
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No. 6.1e-172;
smatches 7;
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                                      Claim 1; Page 108-110; 132pp; English.
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llarity 98.0%;
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Matches 586; Conserv
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Neisseria meningitidis strain H15.
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                                                                                                                                                                     Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                    present invention.
                                                                                                                                                                            WPI; 2001-488774/53.
N-PSDB; AAS09167.
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DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 356
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                               PYORTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ----
                                                                                                                                                                                                                                                                                     SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
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                                                                                                                                                                                                                        PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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7; Indels
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 Mismatches
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 Matches 586; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunoreactive peptide
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N-PSDB; AAX85790.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to the isolation of novel Neisseria
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Pred. No. 6.1e-172;
                                                       /label= C2
/note= "Conserved region 2"
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                                                                                                                                             /note= "Variable region 1"
                                                                                                                                                                                                                                                                                                                                                                /label= C4
/note= "Conserved region
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/label= V2
/note= "Variable region
                                                 Location/Qualifiers
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/note= "Variable
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/note= "Variable
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98.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitidis which is approximately 62 kba. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to be used to learn if we work to the proteins and antibodies can also be used to identify immunoreactive peptides.
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                                                                                 present sequence represents a surface protein of Neiserria
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                                                                                                                                                                                                                                                                     Length 598;
             surface proteins useful for treating
                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 1.5e-170;
2; Mismatches 10;
                                                   Claim 1; Page 91-93; 132pp; English.
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Best Local Similarity 97.3%;
Matches 582; Conservative
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                            infections
             meningitidis
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             Neisseria
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AMUOGISE2-AMUGISE6. The modified or mutant Nhha Polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain B210 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
          Surface antigen NhhA; meningococcal disease; meningitis vaccine
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/label= C1
/^nte= "Conserved region 1"
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/note= "Conserved region 2"
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/note= "Variable region 3"
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/note= "Conserved region
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/note= "Variable region
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                                                             Location/Qualifiers
                                   Neisseria meningitidis strain B210.
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/note= "Variable
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N-PSDB; AAS09168.
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the present invention

AA;

Sequence

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treating

surface proteins useful for

Claim 1; Page 100-101; 132pp; English

infections meningitidis

meningitidis

Neisseria

WPI; 1999-418754/35. N-PSDB; AAX85792.

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                                                              PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ---- 116
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                 Gaps
                               1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
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                                       NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
                                                                                                                                  SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
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 Length 598;
                 Indels
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2948; DB 22;
No. 1.5e-170;
                10;
                                                                                                                                                                                                                                                                                                                                                                                                                    surface protein of Neisseria meningitidis.
                 2; Mismatches
Score 2948;
Pred. No. 1.
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         97.38;
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                 Conservative
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          Similarity
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Best Local S
Matches 582
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Length 594;

594 AA;

Sequence

The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

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                                                                                                                                                                                    DEVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG
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                  Indels
95.1%; Score 2874; DB 20; 95.6%; Pred. No. 4.5e-166;
                  5; Mismatches
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Query Match 95.1
Best Local Similarity 95.6
Matches 568; Conservative
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This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the serogroup B strain ATCC13090. The BASB029 protein is homologous to the themophilus influenzes surface fibril (HSP) protein. The invention relates to BASB029 polynucleotide sequences (AAX57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynuclectide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 comply pacterial infections. The protein is useful in the combinant correction is useful for treating in the combinant correction is useful for the stimulation of the immune system of an organism
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                                                 BASB029; Nisseria meningitidis: surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
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               BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
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                                                                                                                                                                                /note= "Encoded by AATC"
                                                                                                                                                                                                                                                                                                                                                                   SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Fig 2; 74pp; English.
                                                                                                                                                                                                                                                                                              99WO-EP03255.
                                                                                                                                                                                                                                                                                                                              98GB-0010276.
                                                                                                       Weisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ39864
                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                            07-MAY-1999;
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                                                                                                                                                                                                                                                         18-NOV-1999
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SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
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                                                                                                                                                  PVRITHVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                      DEVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG
                                                                                                                                                                                                                                                                                         N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                       Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                 /label= C1
/ante= "Conserved region 1"
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/note= "Conserved region 3"
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/note= "Conserved region 5"
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/note= "Variable region 1"
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/note= "Variable region 4"
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/label= C2
/note= "Conserved region
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/note= "Variable region
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/note= "Variable region
                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis strain EG327
                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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/note= "Conserved
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                                                                                                                                                                                                  The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AMU06182-AMU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in Spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen. The present sequence representing the wild type surface antigen. From N. meningitidis strain EG327 is 1 of 10 NhAA polypeptide sequences (AAU06111-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVQRTAVVLSFRSDKEGTGGKEGTEDSWWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 594;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                Score 2874; DB 22;
Pred. No. 4.5e-166;
; Mismatches 21;
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                                                                                                                                                                                 Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                95.1%;
95.6%;
                     25-JAN-2001; 2001WO-AU00069
                                         25-JAN-2000; 2000US-0177917
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                               (UYQU ) UNIV QUEENSLAND
                                                                                    Jennings MP;
                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                       2001-488774/53
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                 594 AA;
                                                                                                                   N-PSDB; AAS09164.
02-AUG-2001.
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PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                            1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                   594
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                                                                                                 541 KSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                           Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.7%; Score 2802.5; DB 20; Lengt
92.5%; Pred. No. 9.6e-162;
live 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    surface protein of Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jennings MP, Moxon ER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-DEC-1997;
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25-JAN-2001; 2001WO-AU00069 25-JAN-2000; 2000US-0177917

WO200155182-A1. 02-AUG-2001 UYQU ) UNIV QUEENSLAND Peak IRA, Jennings MP;

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360
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                                                                                                          AYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
         DPTVHLNG1GSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWN1KGVKPGTT
                                 ASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVK IGAKTSV I KEKDGKLVTGKG
                                                                 KDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
                                                                          KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                  KDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                                                                                                                                                                                                                                              Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                             meningitidis H38 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Conserved region 3"
196..217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= C4
/note= "Conserved region 4"
                                                                                                                                                                                                                                                                                                                                                                                        "Conserved region 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Variable region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Variable region 4"
                                                                                                                                                                                                                                                                                                                                                                                                                               /label= C2
/note= "Conserved region
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/note= "Conserved region
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/note= "Variable region |
132..195
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                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis strain H38
                                                                                                                                                                                                                                                            AAU06176 standard; Protein; 599
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/label= C3
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/label= C1
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/label- v1
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhh AAMU06182-AAMU06186). The modified or mutant Nhhh polypeptides are characterised by deletions of non-conserved mino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhhh from N. meningitidis strain 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 -NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 EPVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ--- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 DPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 599;
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Pred. No. 9.6e-162;
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                                                                                                                                                                                                                                                                                       Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 92.7
Best Local Similarity 92.5
Matches 554; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the present invention.
                                                                                                                                                                               WPI; 2001-488774/53
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361

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KGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK

KDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG

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Amino acid
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                                                                                                                                                                                                                                                                                                                                        BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis; infection; treatment; prevent; antibacterial drug.
                                   535
421 gkmdetvninagnnieitrngknidiatsmtpqfssvslgagadaptlsvddkgalnvgs 480
                               New polypeptide from neisseria meningitidis useful for diagnosis, treatment or prevention of bacterial infections in mammal
                                                                                               536 AYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                                                                                                                                                                                                                                                                                                          BASB029 amino acid sequence from N. meningitidis strain H44/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by AATC"
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                                                                                                                                                                                                            AAY57045 standard; Protein;
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N-PSDB; AAZ39865.
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                                                                                                                                                                                              AAY57045
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the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynuclectide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynuclectides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 YLEPVQRTAVVLSFRSDKEGTGEKEGT-EDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; pharmaceutical; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 KMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSK
                                                                                                                                                                                                                                                                                           Length 591;
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                                                                                                                                                                                                                                                                                           21;
                                                                                                                                                                                                                                                                                           Score 2750.5; DB 2
Pred. No. 1.3e-158;
8; Mismatches 26;
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                                                                                                                                                                                                                                                                                              91.0%;
92.5%;
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                                                                                                                                                                                                                                    591 AA;
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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD----DDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLEPVQRTAVVLSFRSDKEGTGEKEGTED - SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537 YLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
                           Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                            Surface protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.7%; Score 2740.5; DB 20
92.1%; Pred. No. 5.3e-158;
live 11; Mismatches 25;
                                                                                                                                                                                 surface protein of Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 127-128; 132pp; English.
                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           IRA;
                                                                                                      591
                                                                                                                                                                                                                                                                                                                                                                                                                          Peak
                                                                                                    AAY23746 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                        97GB-0026398
                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      meningitidis infections
                                                                                                                                                                                                                                                                                                                                                                                                (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                                                          Immunoreactive peptide.
                                                                                                                                                                                                                                                   Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                           Moxon
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Matches 551; Conserv
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                                                                                                                                                                                                                                                                                                   The invention provides proteins (AAY27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) encoding the proteins. Compositions comprising the protein, nucleic acid or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             295 gengsstdegeglvtakevidavnkagwrmktttangqtgqadkfetvtsgtnvtfasgk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o and its nucleotide sequence, useful in vaccines or compositions for treating and/or preventing Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 90.7%; Score 2740.5; DB 20; Lengtl
Local Similarity 92.1%; Pred. No. 5.3e-158;
les 551; Conservative 11; Mismatches 25; Indels
                                                                                                                                                         Scarlato
                                                                                                                                                         Rappuoli R,
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                                                                                                                                                                                                                                                                           1; Page 62; 123pp; English.
                                                                                                                                                         Pizza
                                                                          98GB-0002143.
98GB-0000760.
98GB-0019015.
                                                   99WO-IB00103
                                                                                                                                                        Masignani V,
                                                                                                                                                                                                                                                  meningitidis infections
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WO9936544-A2
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01-SEP-1998;
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                                                                                                                                 DINKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 536
                                                                                                                                                                   175 ttvhlngigstltdtllntgattnvtndnvtddekkraasvkdvlnagwnikgvkpgtta
                          DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK
                   SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
                                                                                                                                                                                                                                                                                                                              antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                                                                              N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Predicted mature protein, specifically
claimed in claim 12"
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/note= "Variable region 3"
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/note= "Variable region 4"
237..591
                                                                                                                                                                                                                                                                                                                                                                                                                                     "Variable region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              //abel= V2
/note= "Variable region 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= C2
/note= "Conserved region
                                                                                                                                                                                                                                                                                                                                                                                                           "Conserved region
                                                                                                                                                                                                                                                                                                                                                                         1..51
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                            52..591
/label- Mature_NhhA
                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis strain PMC21
                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/note= "Conserved
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                                                                                                                                                                                                                                                                                                                                                                                                                 51..108
/label= v1
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/label= C1
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meningtidis mutant polypeptides of the surface antigen Nhha characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningtidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningtidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen from N. meningtidis strains than present sequence representing the wild type surface antigen. The present sequence representing the wild type surface antigen Nhha from N. meningtidis strain pw221 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningtidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176
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                                                                                                                                                                                                                                                                                                                               or
                                                                                                                                                                                                                                                                                                           New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANCNKVNITSDTKGLNFAKETAGTNGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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92.1%; Pred. No. 5.3e-158;
ive 11; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to the isolation of novel
              'n
              /note= "Conserved region
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                                                                                                                                                     2000US-0177917.
                                                                                                                    25-JAN-2001; 2001WO-AU00069
/label= C5
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                                                                                                                                                                                         (UYQU ) UNIV QUEENSLAND.
                                                                                                                                                                                                                           Peak IRA, Jennings MP;
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                                                                                                                                                      25-JAN-2000;
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hes 551;
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GenCore version 4.5
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OM protein - protein search, using sw model

July 3, 2002, 08:37:10 ; Search time 39.66 Seconds (without alignments) 365.830 Million cell updates/sec Run on:

US-09-771-382-9 3023 1 MNKIYRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 594 Title: Perfect score: Sequence:

BLOSUM62 Gapoxt 0.5 Scoring table:

231628 segs, 24425594 residues Searched:

231628 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued\_Patents\_AA:\* Database :

1: /cgn2\_6/ptodata/2/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/laa/6A\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/laa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/laa/pcTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/laa/pcTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

•		di			SUMMARIES		
Result No.	Score	Query	Duery Match Length DB	DB	ID	Description	
-		000	704	-		i	
-	2063	7.00	124	r	1-CCT-//C-60-CO	sednence // Appri	
7	3023	100.0	594	4	US-09-669-974-7	Sequence 7, Appli	
٣	2971	98.3	598	4	US-09-377-155-13		
4	2971	98.3	598	4	US-09-669-974-13	13	
2	2948	97.5	598	4	US-09-377-155-5	'n	
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7	2874	95.1	594	4	US-09-377-155-9	6	
8	2874	95.1	594	4	US-09-669-974-9	0	
6	2802.5	92.7	599	4	US-09-377-155-15	15,	
10	2802.5	92.7	599	4	US-09-669-974-15	15,	
11	2740.5	90.7	. 591	4	US-09-377-155-21	21,	
12	2740.5	90.7	591	4	US-09-669-974-21	21,	
13	2733	90.4	592	4	US-09-377-155-2	2, A	
14	2733	90.4	592	4	US-09-669-974-2	7	
15	2721.5	90.0	591	4	US-09-377-155-11	Sequence 11, Appl	
16	2721.5	90.0	591	4	US-09-669-974-11 .	11	
17	2664	88.1	592	4	US-09-377-155-17	17,	
18	2664	88.1	592	4	US-09-669-974-17	17,	
19	2573.5	85.1	583	4	US-09-377-155-19	19,	
20	2573.5	85.1	589	4	US-09-669-974-19	19,	~
21	1330.5	44.0	2353	4	US-09-377-155-33	33,	
22	1330.5	44.0	2353	4	US-08-913-942-4	4, 4	
23	1330.5	44.0	2353	4	US-09-669-974-33	33	
24	1329.5	44.0	2354	4	US-09-268-347-47	47,	
25	1295.5	42.9	2411	4	US-09-268-347-36	36,	
26	1263	41.8	607	-	US-08-409-995-6	Sequence 6, Appli	
27	1263	41.8	607	æ	US-08-685-467-6	9	

Sequence 6, Appli	Sequence 4, Appil	Sequence 32, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 32, Appl	Sequence 2, Appli	Sequence 32, Appl	Sequence 44, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	15,	Seguence 26, Appl	24, 1	Sequence 30, Appl	Sequence 28, Appl
US-08-913-942-6	US-08-409-993-4 US-08-685-467-4	US-09-268-347-32	US-08-409-995-2	US-08-685-467-2	US-09-377-155-32	US-08-913-942-2	US-09-669-974-32	US-09-268-347-44	US-08-409-995-5	US-08-685-467-5	US-08-913-942-5	US-08-913-942-15	US-09-268-347-26	US-09-268-347-24	US-09-268-347-30	US-09-268-347-28
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28	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 416
  301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 360
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Matches 586,
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TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
                                                                                                              DEVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG
                                                                                                                                                   PVRITHNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                                         TVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
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; Pred. No. 8.7e-236;
0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1090-09-26
PRIOR PELICATION NUMBER: US 09/377,155
PRIOR PELICATION NUMBER: US 740198/01031
PRIOR PELING DATE: 1999-08-19
PRIOR PELING DATE: 1999-12-14
PRIOR PELING DATE: 1999-12-14
PRIOR PELING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                               APPLICANT: PEAK, Ian Richard Anselm
                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
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100.0%;
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Best Local Similarity 100.
Matches 594; Conservative
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421 TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
                                                                                                                                                                                 PVRITHVVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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                                                                               TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK
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llarity 98.0%; Pred. No. 1.4e-231;
Conservative 1; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INCOMPATION:
APPLICANT: PERK, Ian Richard Anselm
APPLICANT: PENNINGS, Michael Paul
APPLICANT: BUNNINGS, Michael Paul
APPLICANT: BONNINGS, Michael Paul
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
PRIOR FILING DATE: 1997-12-12
SOFTWARE: PatentIn Ver. 2.0
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; Sequence 13, Application US/09377155
; Patent No. 6197312
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NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
                                                                                                                                                      YLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
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                                          PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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                            KMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSK
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Pred. No. 9.9e-230;
2; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR PLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                 APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE AN
                                                                                                                                                                                                                                        Sequence 5, Application US/09377155
Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Neisseria meningitidis US-09-377-155-5
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Best Local Similarity 97.3%;
Matches 582; Conservative
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SOFTWARE: Patentin Ver. 2.0
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Pred. No. 1.4e-231;
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-14
PRIOR PELICATION NUMBER: PCT/AU98/01031
PRIOR PLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                             APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                     Sequence 13, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Neisseria meningitidis US-09-669-974-13
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98.0%;
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SOFTWARE: PatentIn Ver. 2.0
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Matches 586; Conserv
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US-09-669-974-13
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Pred. No. 9.9e-230;
2; Mismatches 10;
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                                                                                                                                                                                                Sequence 5, Application US/09669974
Patent No. 6333173
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97.3%;
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Pred. No. 9.1e-224;
5; Mismatches 21;
                                                                                                                                                                                                                                                                              Sequence 9. Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENK, Ian Richard Anselm
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
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Best Local Similarity 95.6%;
Matches 568; Conservative
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SOFTWARE: Patentin Ver.
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                                541 KSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW
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                                                                                                                                                                                 APPLICANT: DEBK, Tan Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT RAPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
                                                                                                                                         ; Sequence 15, Application US/09377155
; Patent No. 6197312
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             NUMBER SOFTWARE: Pate SEQ ID NO 15
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Pred. No. 9.1e
5; Mismatches
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APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1999-12-12
NUMBER: OF SEQ ID NOS: 33
SOFTWARR: PECHLIN Ver: 2.0
                                                                                                                                                    Sequence 9, Application US/09669974
Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Neisseria meningitidis US-09-669-974-9
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Best Local Similarity 95.6%;
Matches 568; Conservative
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US-09-669-974-9
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Pred. No. 5.4e-218;
12; Mismatches 28;
                                                                                                                                                                                                                                            APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Ian Richard Paul APPLICANT: DENNINGS, Michael Paul APPLICANT: MOXON, E. Richard FILL OF INVENTION: NOVEL SUBFACE ANTIGEN FILE REFERENCE: 065064/0128 CURRENT APPLICATION NUMBER: US/09/669,974 CURRENT FILING DATE: 1999-08-19 PRIOR FILING DATE: 1999-08-19 SOFTWARE: PARIOR PRIOR PRIOR PRIOR PRIOR FILING DATE: 1997-08-16 SOFTWARE: 1997-08-19 SOFT
                                                                                                                                                               Sequence 15, Application US/09669974 Patent No. 6333173
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Best Local Similarity 92.5%;
Matches 554; Conservative 1
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                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BERK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MONON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT FILLING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: 1099-08-19
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
                               Sequence 21, Application US/09377155 Patent No. 6197312
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SOFTWARE: Pate
SEQ ID NO 21
RESULT 11
US-09-377-155-21
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Best Local $
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; Pred. No. 5.3e-213;
11; Mismatches 25;
                                                                                APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVEXTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION WUMBER: US/09/669,974
CURRENT FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: CB 9726398.2
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-14
PRIOR FILING DATE: 1997-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
                                 Sequence 21, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Neisseria meningitidis US-09-669-974-21
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92.18;
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Best Local Similarity 92.1%
Matches 551; Conservative
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LENGTH: 591
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Pred. No. 2.2e-212;
Sequence 2, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: PEAK, Ian Richard Paul
APPLICANT: MOXON, E. Richard
TILE OF INVENTION: NOVEL SURPACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT APPLICATION NUMBER: PCT/AU98/01031
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                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: GB 9
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
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Best Local Similarity 91.8%;
Matches 550; Conservative 1
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LENGTH: 592
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PEAK, Ian Richard Anselm

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APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR PRLICATION NUMBER: CT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-12
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SOFTWARE: Patentin Ver. 2.0
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LENGTH: 591
  APPLICANT:
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91.8%; Pred. No. 2.2e-212;
iive 10; Mismatches 27;
                 APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: JENSON, JENSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Neisseria meningitidis
US-09-669-974-2
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GENERAL INFORMATION:
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Best Local Simi
Matches 550;
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                                                                                                                                               58 YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ
                                                                                                                                                                                                                      117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
                                                                                                                                                                                                                                                                                             177 PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
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                                                                      1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD---DDDL
                                  11;
 Length 591;
                                    27; Indels
 DB 4;
Query Match 90.0%; Score 2721.5; DB 4 Best Local Similarity 91.6%; Pred. No. 1.8e-211; Matches 548; Conservative 12; Mismatches 27;
                                                                                                                                                                                  61
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3, 2002, 08:37:11

completed: July he: 337 sec

US-09-377-155-11 ; Sequence 11, Application US/09377155 ; Patent No. 6197312

Patent No. 6197312 GENERAL INFORMATION:

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GenCore version 4.5
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OM protein - protein search, using sw model

July 3, 2002, 08:38:24; Search time 58.79 Seconds (without alignments) 970.863 Million cell updates/sec Run on:

US-09-771-382-9 3023 1 MNKIYRIIWNSALNAWVVVS.....TASGNSRGHFGASASVGYQW 594 Title: Perfect score: Sequence:

283138 seqs, 96089334 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	adhesin NMB0992 [i	probable surface f	adhesin homolog HI	surface protein XF	surface protein XF	probable autotrans	probable adhesin Z	probable adhesin E	probable surface p	surface-exposed on	hypothetical prote	adhesin AIDA-I pre	probable adhesin h	probable autotrans	AidA-I adhesin-lik	probable adhesin Z	hypothetical prote	hypothetical prote	~	probable RTX famil	surface-array prot	ydeK protein - Esc	hypothetical prote		æ	probable adhesin P	hypothetical prote	puative autotransp	S-layer protein -
SUMMARIES	£ £	G81133	A81888	164138	D82671	A82615	AC0976	A86036	<b>Н91188</b>	AH0110	C82672	G64964	S28634	AF0394	AD0123	D90803	н85611	T31105	F90696	D85724	B85547	A56143	A64905	E90893	A83080	A43855	H83135	B98047	AD0548	T03415
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æ	Query	90.7	84.4	21.0	13.4	13.0	12.3	11.8	11.8		8.6	7.9	7.6	7.3	7.2	7.1	7.1	7.1	7.0	6.9	6.8	9.8			6.8	6.7	6.7		9.9	9.9
	Score	2740.5	2552	635	404	392.5	371	356	356	338	260	240	230	221.5	217.5	216	216	213.5	211	207.5	207	206.5	206.5	204.5	204.5	204	203	201	200.5	199
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AB0480	A28182	A41477	AI0452	S41525	B43855	AH2515	S76109	140711	T33369	AG2560	C48399	E97835	F90961	F85809	S11672
71	N	7	C3	7	7	~	7	7	7	7	7	7	7	7	7
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9.9	6.5	6.5	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.3	6.2	6.2	6.2	6.2
199	198	197.5	197	196	195.5	195	194	.193	193	192.5	190	188.5	188	188	188
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

 RESULT 1 GB1133 adhesin NMB0992 C;Species: Neis: C;Date: 31-Mar- C;Accession: GB R;Tettelin, H.; Hickey, E.K.; H. Hickey, E.K.; H. Ti, H.; Olin, H.; Authors: Gran, A;Title: Comple A;Reference num; A;Title: Comple A;Reference num; A;Title: Dealin, A;Accession: GB A;Acces	RESULT 1  GB1133  adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  Cispecies: Nelsseria meningitidis  Cibote: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001  CiAccession: GB1133  Scarlato, V.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hicky, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.  Cience 287, 1809-1815, 2000  A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;  A; Reference number: A81000; MUID:20175755  A; Reference number: A81000; MUID:20175755  A; Redecance number: A81000; MUID:20175755  A; Redecance number: AB1000; MUID:20175755  A; Redecance number: BNA  A; Redecances: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722  A; Cross-references: GB:AE002450; GB:AE002098; NID:G7226229; PIDN:AAF41395.1; PID:g722  A; Genetics: NVB0992
 Query Match Best Local Matches 55	Ouery Match Best Local Similarity 92.1%; Score 2740.5; DB 2; Length 591; Best Local Similarity 92.1%; Pred. No. 4.8e-131; Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;
Oy 1 Db 1	1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLEFATVQANATDDDDL 57 ,
Qy 58 Db 61	YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116   :                       :  :     :
Qy 117 Db 121	NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD 176
Qy 177 Db 175	PTVHENGIGSTETDTEENTGATTNVTNDNVTDDEKKRAASVKDVENAGMNIKGVKPGTTA 236
 Oy 237 Db 235	SDNVDEVRTYDTVEFLSADFRTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK 296 
 Qy 297 Db 295	DENGSSTDEGECLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFETVTSGTNVTFASGK 356 

357 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKG 416

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LNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
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A;Residues: 1-592 <PAR>
A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
A;Experimental source: serogroup A, strain 22491
C;Genetics:
                                                                                                                                                                                                                                             probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2249
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                    S.R.; Morel
Rajandream,
                                                                                                                                                                                                                                                                                     C; Accession: A81888
R; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandrean Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556
A;Accession: A81888
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                                                                                                                                                  YLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                             EPVQRTAVVLSFRSDKEGTGEKEG-----TEDSNWAV--YFDEKRVLKAGAITLKAGDNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIKQNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTA -- SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TFASGRGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGN
                                       KMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.4%; Score 2552; DB 2;
86.8%; Pred. No. 1.5e-121;
tive 16; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: NMA1200
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Best Local S
Matches 524
              355
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dunestin concloses Haemophilus influenzae (Strain No. N. 20)
C. Species: Haemophilus influenzae
C. Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C. Species: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C. Scassion: 164138
C. Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A.Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A.Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A. Reference number: A64000; MUID:95350630
A. Reference number: A64000; MUID:95350630
A. Scassion: I64138
A. Status: nucleic acid sequence not shown; translation not shown
A. Wolecule type: DNA
A. Wolecule type: DNA
A. Residues: 1-298 <TIGRN
A. Residues: 1-298 <TIGRN
A. Residues: 1-298 <TIGRN
A. Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:H11732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 -DQGGKSVTFALAKDLDVKTAKVSDTLTIGGNTPAAGGATPKVSITSTADGLKLAK---G 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAG-AITLKAGDNLKIKQNTN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66
1 MNKIYRIIWNSALNAWVVVSELFRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ENTNDSSFTYSLKKDLTDLTSVETEKLSFGAN-----GNKVNITSDTKGLNFAKETAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 TNGDPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            531 AGLVQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNKIFKVIWNVVTQTWVVVSELTRAHTKRTSATVATAVLATVLSATVQA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 21.0%; Score 635; DB 2; Length 29 Best Local Similarity 47.6%; Pred. No. 2.9e-25; Matches 151; Conservative 42; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                adhesin homolog HI1732 - Haemophilus influenzae (strain Rd
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Risperimental Source: strain 945

Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Brones, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Franca, S.C.; Franca, B.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigima, J.D.; Junqueira, M.A.; Madeira, A.M.B.N.; Martins, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.P.; Authors: da Silva, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A. Teshako, M.H.; Vallada, H.; Van Silva, A.M.; Silva Jr., W.A.; da Silvai, A.M.; Salvaiak A.R.; Feference number: A59328
                                                                     A.Residues: 1-2059 <SIM>
A.Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1395 SGVTAGTEETD-AVNFSQLKSISTAVDQGWTLTASGANGSKVASGGTVDLKNTDGNLTIS 1453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1747 GVGTQASGEGAAAVGSGAAASGKGSTAIGRNAIASADGSVALGDGAKDGGRGAESYTGKY 1806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KAGDNLKIKQNTNENTNDSSFTY---SLKKDLTDLTS---VETEKLSFGANGNKVNITSD 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------KRVLKAGAITL------ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 TKGLNFAKETA----GTNGDPTVHLNGI-----GSTLTDTLLNTGA--TTNVT----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 DNVTDDEKKRAASVKDVLNAGWNI-----KGVKPGTTASDNVD-----FVRTYDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 VEFLSADTK-----TTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1631 VFNLSKDFKVDEVTAGNTVVNTDGVKVG--SDVSLGAMGLFI--ANGPSVTASGFNAGDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----GSSTDEGEGLVTAKEVIDAVNKAGWRWKTTT------ANGQTGQ---AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 KFETVTSGTNV-----TFASGKGTT-----ATVSKD------DQG----NITVKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DALNVNQL----QNSGWNLDS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1807 SGVQNNTVGTVSVGDAAKGETRSISNVADAKEAMDAVNLRQLDAVAQKSNLQTDDMRHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KAVAGSSGKVISGNVSPSKGKMDETVNINA---GNNIEITRN----GKNIDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 ATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKGVAQNLNNRIDNVDGNAR----AGIAQAIATAGLVQAYLPGKSMMAIGGDTYRGEAGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.4%; Score 404; DB 2; Length 2059; 24.8%; Pred. No. 1.5e-12; ive 98; Mismatches 214; Indels 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  558 AIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
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Best Local Similarity 24.8's
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Contents: annotation
C;Genetics:
A;Gene: XF1529
A;Accession: D82671
A;Status: preliminary
A;Molecule type: DNA
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A; Experimental source: strain 9a5c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acenclo, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, E.E.; La chado, M.A.; Madeira, A.M.B.N.; Madeira, M.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Balmieri, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A; Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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A; Status: preliminary
A; Molecule type: DNA
A; Molecule: 1-1190 ASIM>
A; Residues: 1-1190 ASIM>
A; Cross-references: GB: AE004017; GB: AE003849; NID: 99107083; PIDN: AAF84783.1; GSPDB: GN
                                                                                                                                                                                                                                                              Surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Mug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: AB2615
R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: AB2515; MulD:20365717
A;Note: for a complete list of authors see reference number A59328 below
RESULT
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for Nucleotide

28; 365 DDQGNITVKYDVNVGDALNVNQL----QNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE 420 47 VQANATDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITL 106 905 IGRNAVASADGSVALGD-GAKDGARGAESYTGKYSGLQNNTVGTVSVGDASKGETRTVS- 962 YD-----GGTQGGNYNGDGATGTRSIAVGVGTLASA----EGATAVGSGAAASGKGSTA 305 EGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSK 572 VAAGTADTDAVNFSQLQ...-AVSSTASKGWNLLASGANSSN...--VVPGESVDL ----KETAGT----NGDPTVHLNGIGS-----TLTDTLLNTGATT---NVTNDN--799 LVITDGPSVTSSGI----NAGSQKITNVAAGTADTDAVNLSQLNTAMAGSGAKSVHYYST YDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGKDENG-SSTD 619 KNSDGNLLITKTTDSNDVTFNLATALKVDSLTTGNTAMTTDGVTVGSNVTLGSTGLVITD Indels 195; Length 1190; 107 KAGD-NLKIKQNTNENTNDSSFTYSLKKD--LTDLTSVETEKLSFGAN----Query Match
13.0%; Score 392.5; DB 2;
Best Local Similarity 24.7%; Pred. No. 2.9e-12;
Matches 168; Conservative 88; Mismatches 230; --VTDDEKKRAASVKDVLNAG-WNIKGVKPGTTASD-------GNK--VNI---TSDTKGLNFA----168 206 246 855 152 셤 õ 음 Qγ qq δ d ò g οy q ò g ö

Qy       349 NVTFASGKGTTATVSKDDQGNIT	Db 932RITHNYAGVNNTDAVNVAQIKASEAGSVRYETNADGSVNRSULALGDGSGGTTRIGNV 989  Qy 504GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA 536	A; Status: preliminary A; Status: preliminary A; Molecule type: DNA A; Rolecule type: DNA A; Gene: 25029 A; Gene: 25029 A; Gene: 25029 A; Gene: 25029 A; Conservative 81; Mismatches 240; Indels 108; Gaps A; Gene: 25029 A; IN MIKIGNTNENTDSSFTYSLKKDITDLISVETEKLSFCANGNKVNITS 159 A; IN MIKIGNTNENTDSSFTYSLKKDITDLISVETEKLSFCANGNKVNITS 159 A; IN MIKIGNTNENTDATY-IQENGAGINYVRTNDDCLAFNDASAQCYGATAIGYNS 1083 A; IN MIKIGNTNENTDATY-IQENGAGINYVRTNDDCLAFNDASAQCYGATAIGYNS 1083 A; IN MIKIGNTTANGWNIKGYREGINGSSTYDGELL 1143 A; IN MIKIGNT
Db 963NVADAKEATDAVNLRQLDRVAQDANRYVDNKIESLSEGGTF 1003  Qy 421 TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEG 469	transporter sapB [imported] - Salmonella enterica s lmonella enterica subsp. enterica serovar Typhi species has also been called Salmonella typhi species has also been called Salmonella typhi species. Bas also been called Salmonella typhi ACO976 ACO976 ACO976 ACO976 ACO976 ACO976 ACO (Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd S.; O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd S.; O'Gaora, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd AF 852, 2001 ACO (Gaora, P.; Cronin, M.; Rutherford, K.; Simmonds, M.; Slete genome sequence of a multiple drug resistant Sumber: ABO502; PMID:11677608 ACO976 ACO976 ACOPTO (ACOPTO	Ouery Match  Best Local Similarity 22.0%; Pred No. 3.2e-1; Matches 184; Conservative 105; Mismatches 263; Indels 286; Gaps 31; Matches 184; Conservative 105; Mismatches 263; Indels 286; Gaps 31;  QY 27 TKRASATVATNVLATLLFATVQANATDDDDLXLEPVQRTAVLEFRSDKEGTG 79  DD 286 TNLAAGTLAADSTDANGSQLYETNQKVDQNTSAIADINTSITNLSSDNLSMNETTNSFS 345  QY 80 EKGCTEDSUMAVYFERKRLKAGAITLKAGDNLKIKONT

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Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - Escherichia coli (strain 0157:H7, substrain EDL93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VADGSEAHDAVT-VRQLQNAIGAVATTPTKYFHANST 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ision 16-Feb-2001 #text_change 14-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : | : | : : | | : | CRIGIGYGAYVDANALN---GIAIGSNAQVIHVNSIA 1252
                                                                                                                                                                                                                                                                                         SLGAGADAP-----TLSVDDE-GALNVGSKDTNK 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----NLNNRIDNVDGNARAGIAQAIATAGLVQA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKKDLTDLTSVET -- EKLSF -- -- GANGNKVNITS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GIGSTLTDTLLNTGA-TTNVTNDNV-----TDDEKK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKA 322
-----VKYDVNVGDALNVNQLQN 389
                                | | : | | : : EEDSLAVGTDSLAMGAKTIVNADAGIGIGLNTLVMAD 751
                                                                                                GSQTTRGAQTDYTAYNMDTPQNSVGEFSVGSEDGQRQ 811
                                                                                                                                                                                                                          :::|| ::|
AQVSRNTQSITNLNTQVSNLDTRVTNIENGIGDIVTT 871
                                                                                                                                                                                                                                                                                                                    ASEAGSVRYETNADGSVNYSVLNLGDGSGGTTRIGNV 989
                                                                                                                                                                                             IEITRNGKNI------DIATS 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 356; DB 2; Length 1588;
Pred. No. 2.9e-10;
1; Mismatches 240; Indels 108; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | : | : | | : | | : | | : | | GVSMVSESGGWVYKLQGTSNSQGDYSAAIGAGFQW 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ohemorrhagic Escherichia coli 0157:H7.
21074935; PMID:11206551
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Cipedies: Yersinia pestis
Cipedies: Oz.Nov-2001
Sipedies: Yersinia pestis
Cipedies: Nov-2001
Sipedies: Yersinia pestis
Cipedies: Nov-2001
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Recession: AHOLIO
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain CO92)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175 C; Genetics: A; 
                                                                                                                                                                                                                                   1432 LKSSEAGGVRYDTKADGSIDYSNITLGG-GNGGTTRISNVSAGVNNNDVVNYAQLKQSVQ 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 IGVAAG-----SASSDAVNVAQLIAVGDQVQQN-----TANITSLGGRVTTIE----G 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 SVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKT--- 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---EVKIGAKTSVIKEKDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTT 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 GAGAVAIG--DGAAASADGSVAIGQGSGDNGRGVENYIG-------KYSN 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330 TANGQIGQADKFETVISGINVTFASGKGITATVSKDDQGNIIVKYDVNVGDALNVNQLQN 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 SGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNI-EITRNGKNIDI--ATSMA 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAGAITLKAGDNLKIKQNTNENTNDSSFT-YSLKKDLTDLTSVETEKLSFG-ANGNKVNI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGDTYRGEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165 DNGVGIGNTALVGAAATGGIAIGFGTQVTAAGATAIGSAAQAQGA------QSLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 ASNTSSG-----TVSVGNTAT-----GETRTVSNVADG------LQATDAVNLRQLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNVTN--DNVTDDEKKRAA
                                                                                         QFSSVSLGAGADAPTLSVDDEGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 TKRASATVAT----AVLATLLFATVQ-----ANATDDDDLYLEPVQRTAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 658;
                                                                                                                                                                                                                                                                                                                                                 11.2%; Score 338; DB 2; 23.8%; Pred. No. 7.5e-10; Live 84; Mismatches 236;
                                                                                                                                                                                                                                                                                                                   YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
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Matches 154; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-658 <KUR>
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1253 IGNGSTTTRGAQTNYTAYNMDAPQNSVGEFSVGSADGQRQITNVAAGSADTDAVNVGQLK 1312
                                                                                                                                                                                                                                                                                                                               1432 LKSSEAGGVRYDTKADGSIDYSNITLGG-GNGGTTRISNVSAGVNNNDVVNYAQLKQSVQ 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                     1491 ETKQYTDQRMVEMDNKLSKTESKLSGGIASAMAMTGLPQAYTPGASMASIGGGTYNGESA 1550
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                                                           -NVNQLQNSGWN 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GQAD---KFETVTSGTNVTFASGKG--- 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 LDSKAVAGSSGKVISGNVSPSKGKM---DETVNINAGNNIEITRN---GKNIDIATSMAP 447
                                                                                                                                                                          LDSKAVAGSSGKVISGNVSPSKGKM---DETVNINAGNNIEITRN---GKNIDIATSMAP 447
                                                                                                                                                                                                                                                                                                                                                                                                       ------NLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGDTYRGEAG 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 NLKIKQNT---NENTNDSSFTYSLKKDLTDLTSVET--EKLSF-----GANGNKVNITS 159
                                                                                                                                                                                                                                                                                     QFSSVSLGAGADAPTLSVDDEGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        557 YAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
                                                              --VKYDVNVGDAL-
                                                           -TTATVSKDDQGNIT-----
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Matches 156; Conservative 106; Mismatches 291; Indels 364; Gaps 3	QY 1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANA 51	Db 1 MNKAYSIIWSHSRQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFAVNISGTVSSGG 60	QY 52 TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEGTE85		Qy 86	Db 114 TISTIVNSGGIQRVSSGGVASATNLSGGAQNIYNLGHASNTVIFSGGNQTIFSGGITDST 173	Qy 106 -LKAGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNIT 158	Db 174 NISSGGQQRVSSGGVASNTTINSSGAQNILSEEGAISTHISSGGNQYISAGANATETIVN 233	Qy 159 SDTKGLNFAKETAGTNGDPTVHLNG	Db 234 SGGFQRVNSGAVATGTVLSGGTQNVSSGGSAISTSVYNSGVQTVFAGATVTDTTVN 289	Qy 195 TGATTNVTNDNVTDDEKKRAASVKDVLNAGWIKG 229	Db 290 SGGNQNISSGGIVSETTVNVSGTQNIYSGGSALSANIKGSQIVNSEGTAINTLVSDGGYQ 349	QY 230 -VKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEK 286	Db 350 HIRNGGIASGTIVNQSGYVNISSGGYAESTIINSGGTLRVLSDGYA 395	Ov 287 DGKLVTGKGKD-ENGS323	20/ DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DESCRIPTION DE LA CONTROL DE LA CONT	Qy 324TG 336	Db 456 NSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRGIWYSNFLTAVWSWFPGTASGANVNLSG 515	Qy 337 QADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQ 388	Db 516 RLNAFAGNVVGTILNQEGRQYVYSGATATSTVGNNEGREYVLSGGITDGTVLNSGGLQAV 575	Oy 389 NSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIAT 443	1 :     : :   :   :   :   :   : :   :   : :   :   : :   :   : :   :   : :   :   : :   :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : :   : : : :   : : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : : :   : : : :   : : : : :   : : : : : :   : : : : : :   : : : : : : :   : : : : :   : : : : : :   : : : : : :   : : : : : : :   : : : : : : : :   :	TATA DISTONATION OF THE CONTRACT OF THE CONTRA	SIGNAPOROVI ACTION OF THE STATE	030 ALLEELLI MAALOV SQUARANI VERNOGELERVI SOGIALULI I VNORGELERI DUOGILINGI	4/3VGSKDINKPVRITNVAP		Qy 490 GVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAG 523	Db 756 NVKNGGIIFDSAVVNADMAVNQNAYINISDQATINGSVNNNGSIVINNSIINGNITND 813	Qy 524 IAQAIATAGLVQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGG 568	Db 814 ADLSFCTAKLLSATVNGSLVNNKNIILNPTKESAGNTLTVSNYTGTPGSVISLGGVLEGD 873	Qy 569 NWIIKGTASGNS 580	::        Db 874 NSLTDRLVVKGNTSGQS 890		:	probable adhesin hmwA [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
ZZ8 KGVKPGTTASDNVDFVKTYDTVEFLSADTKTTTVNVE        -   -   -   -   -   -   -   -	Db 229VKPGTVATDTVVNTGAEGGPDAENGDTGQEVRGDAVRTTINKNGRQIVRAEG 280	QY 278 -AKTSVIKEKDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMK 327	Db 281 TANTTVVYAGGDQTVHGHALDTTLNGGYQYVHNG-GTASDTVVNSDGWQIVKNGGVAG 337	Qy 328 TTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVKYDVNVGDALN 383	Db 338 NTTVN-QKGRL-QVDAGGTAINVILKQGGALVTSTAATVTG 376	OY 384 VNOLQNSGWNLDSKAVAGSSGKVISGNVSPSKCKMDETVNINAGNNIEITRNGKNIDIAT 443	Db 377 INRLGAFSVVEGRADNVVLENGGRLDVLT 405	Qy 444 SMAPQFSSVSLGAGADAPTLSVDDGGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLK 503	Db 406S 443	QY 504 GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGDTY 551	Db 444 GAAVSGTRSDGKAFSIG-GGQADALMLEKGSSFTLNAGDFATDTTVNGGLF 493	GNWIIKGTASGN 579	Db 494 TARGGILAGTTLNNGALLTLSGKTVNN 521	DECITE 12		,		R;Benz, I. submitted to the EMBL Data Library, March 1992	A;Reference number: S28634 A;Accession: S28634		A;Cross-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1; PID:g42255 R;Benz, I.; Schmidt, M.A.	Mol. Microbiol. 6, 1539-1546, 1992 A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escheri		A:Status: 012000 A:Status: DNA	A; Residues: 839-1286 SBE2>	A/cross rereferces: EmbL: A00022 A: Experimental source: strain 2787	A; Accession: 528881 A; Molecule type: protein	A;Residues: 50-56 <be3> A:Experimental source: strain 2787</be3>	R;Suhr, M.; Benz, I.; Schmidt, M.A.	A: The state of the AIDA and evidence for the outer A: Defence of the AIDA and evidence for the outer A: Defence of the AIDA and Evidence for the outer A: Defence of the AIDA and Evidence for the outer A: Defence of the AIDA and Evidence for the outer A: Defence of the AIDA and Evidence for the outer A: Defence of the AIDA and Evidence for the outer A: Defence of the AIDA and Evidence for the outer A: Defence of the AIDA and Evidence for the outer A: Defence of the AIDA and Evidence for the OIDA and Evidenc	Ayecession: 372657		A; Experimental source: DAEC strain 2787 C; Genetics:	A;Genome: plasmid pIB6 C;Keywords: membrane protein	F;1-49/Domain: signal sequence #status predicted <sig> F;50-1286/Product: adhesin AIDA-I #status predicted <mat></mat></sig>	

C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001 C;Accession: AF0394

Query Match 7.6%; Score 230; DB 2; Length 1286; Best Local Similarity 17.0%; Pred. No. 0.0005;

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R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                             A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0394
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1910 <KUR>
A;Cressreferences: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175
A;Genetics: A;Gene: hmwA
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                                                                                                                                                                                                                                                                                      Length
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; Pred. No. 0.0022;
86; Mismatches 271;
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                                            probable autotransporter protein yapH [imported] - Yersinia pestis (strain C092) C;Species: Yersinia pestis C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
RESULT 14
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AD0123

--SISDGGNWIIKGTASG 578

C; Accession: AD0123

R; Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001

A; Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; WUID:21470413; PMID:11586360

A; Accession: AD0123

A; Reference number: AB001; MUID:21470413; PMID:11586360

A; Residues: 1-3705 < KUR>
A; Residues: 1-3705 < KUR>
A; Residues: 1-3705 < KUR>
A; Cometics: C 36; DIDALDLLVNGTAITSGTQGVQSAIQQGGSTVANAIHNYGLASSNSNGDSGLYVNYTLSA 1087 562 452 910 : || : || : || VNLTKTTFALSADNAAALASATLKLSDDSVTTVGTTDRTLHGLDLSGGTLIFDGAVPQSQ 970 515 635 | | : ::: | : : : : : | : SSSQSNDVINLGDGNNSVTIQNGATVSSIITGNGNDFFIINGMSVGSTYLGSLD-AGTGL 748 350 808 392 477 AGDITAATGISATHNGTGTVKIKNDGTITSTTAGIAISSASIKEISVDNTDGTITATAGT 458 111 NLKIKQ-----ANTNENTNDSSFTYSL-KKDLTDLTSVETEKLSFG---ANGNKV 155 809 ILHATLGAGTGSAIVNNSANVSLEQASMFAGTWQVNQGGALTASNSNQLGSAKIGLDGTL 868 364 NVIYNLGTGSILKA------TNTGILAT------KNANNASDIYIRS NKIYRIIWNSALNAWVVVSELFRNHTKRASATVATAVLATLLFATVQANATDDDDLYLEP NTLNFNASTDELAAATSLOGFTNINLVDSHITLVSDDNIGSGMVNIDSSSELLFGSTFDG NLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSV NLDNIAL --- FNHVLTGNGT ------LNVAKNLATTA ---- FDFGSTVGGAFSGI NARA-----GIAQAIATAGLVQAYLPGKSMMA-----IGGDTYRGEAGYAIGYS---VQRTAVVLSFRSDKEGTG----EKEGTEDSNWAVYFDEKRVLKA------GAITLKAGD GVNVLASAILNLFGGTINTSATANGITFAGTEGGHTLTDLT---INLLGTGIALSNVAGV -----GATTNVTNDNVTDDEKKRAASVKDVLNAGWNI-KGVKPGTTASDNVDF-VRTYD INVNGAGIGIQATGGGVNLSASNLIINVANTLGTALQITDGIDNTTTIGNEIQLNAENAT TVEFLSADTKTTTVNVESKDNG--KKTEVKIGAKTSVIKEK---DGKLVTGKGKDE---------NGSSTDEGEGLVTAKEVIDAVNKAGWRM ----TFASGKGT-----TATVSKDDQGNITVKYDVNVGDAL---NVNQLQNS----GW -----SLGAGAD-----APTLSVDDEGALNVGSKD------SLGAGAD-------TNVAQLK----GVAQNLNNRIDNVDG NITSDTKGLNFAKETA------GTNGDPTVHLN--GIGSTLTDTLLNT----277; Length 3705; Indels KTTTANGQTGQ--------ADKFETVTSGTNV-----7.2%; Score 217.5; DB 2; Similarity 20.6%; Pred. No. 0.0083; 85; Mismatches 272; Conservative TNKPVRITNVAPGVKEGDV-164; Query Match Best Local S Matches 164 156 576 749 1028 62 459 196 248 299 069 327 351 393 869 453 911 478 971 519 Q ò q ò qq οy q ò g ŏ g δ Db Qγ qq ŏ g Q g δ ò 셤

3, 2002, 08:38:32

Search completed: July Job time: 303 sec

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1088 LELLADGADALLLATESG 1105
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26; 260 261 VNVESKDNGKKTEVKIG-AKTSVIKEKDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAV 319 347 ----SGGALIADSGATV 396 467 EGINASGKFSIDGTSGQASGLLLE---NG------GSFTVNAGGQAGNTTVGH 440 EGALNV-----GSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNA 520 61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120 121 NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKV----NITSDT------KGLN--FA 167 168 KETAGTNGDPTVHLNGI-------GSTLTDTLLNTGATTNVTNDNVTDDEK 211 -----VQGTAESTTINKNGRQIILFSGLARDTLIYAGGDQSVHGRALNTT 252 348 TNVTFASGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVI 407 Gaps 1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60 212 KRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTY-----DTVEFLSADTK-----TTT SGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDD Query Match 7.1%; Score 216; DB 2; Length 949; Best Local Similarity 21.7%; Pred. No. 0.0017; Matches 132; Conservative 72; Mismatches 211; Indels 194; 368 TLAVSAGGKATSVTIT------| :::|:| NAALSRAVA 499 RAGIAQAIA 529 C;Genetics: A;Gene: ECs1396 86 208 253 408 397 468 441 521 55 ò a δ g ò QQ ò g δ οp οy qq ò g ò qq δ g ô q à

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 3, 2002, 08:48:58; Search time 29.79 Seconds (without alignments) 772.051 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-771-382-9 3023 1 MNKIYRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 594

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTES

Q01837 listeria iv 033479 pseudomonas	P19570 bacillus sp P13390 bacteriopha	P15345 caulobacter	Q01714 rattus norv	P45508 escherichia	084402 cniamydia t P80544 staphylococ	P44969 haemophilus	P45384 haemophilus
P60_LISIV ICEV_PSESX	GUN3_BACS4 VLTF_BPT5	FLEY_CAUCR	SP1_RAT	YFAL_ECOLI	1430_CHLTR MRSP_STAAU	IGAO_HAEIN	IGA2_HAEIN
				Н,		Н	Н
524 1196	825 1396	954	788	1250	1637	1694	1702
5.2	5.2	5.2	5.1	5.1	5.1	5.1	5.1
158.5 158.5	157 156.5	156	155	155	154.5	154.5	154.5
34 35	36	38	40	41	4 4 8	44	45

# ALIGNMENTS

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01-JUN-1994
01-JUN-1994
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Q03155;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                   FEMS Microbiol. Lett. 149:115-120(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%; Score 240; DB 1; Length 1039;
23.7%; Pred. No. 6.7e-05;
ive 57; Mismatches 210; Indels 212; Gaps
                                                               Henderson I.R., Meehan M., Owen P.;
"Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATN -> STI (IN STRAIN ML 308-225).

A -> T (IN STRAIN ML 308-225).

N -> Q (IN STRAIN ML 308-225).

E -> V (IN STRAIN ML 308-225).

S -> N (IN STRAIN ML 308-225).

H -> Y (IN STRAIN ML 308-225).

E -> K (IN STRAIN ML 308-225).

M -> T (IN STRAIN ML 308-225).

GHL -> SHP (IN STRAIN ML 308-225).

S -> P (IN STRAIN ML 308-225).
                                                                                                                                           FUNCTION AS AN ADHESIN.
SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN ML 308-225).
STRAIN ML 308-225).
MNLIYNA (IN STRAIN ML 308-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --> LGA (IN STRAIN ML 308-225).
T (IN STRAIN ML 308-225).
L (IN STRAIN ML 308-225).
                                                                                                                                                                                             SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.
SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SL -> FF (IN STRAIN ML 308-225).
T -> K (IN STRAIN ML 308-225).
W -> L (IN STRAIN ML 308-225).
V -> F (IN STRAIN ML 308-225).
ATN -> STI (IN STRAIN ML 308-225).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTIGEN 43 ALPHA CHAIN.
ANTIGEN 43 BETA CHAIN.
K -> N (IN STRAIN ML 308-225)
SL -> FF (IN STRAIN ML 308-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> TTT (IN REF. 5).
5170D647C8DEEBE0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Signal; Complete proteome.
in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNLVHTS ->
                                                                                                                                                                                                                                                                                                                                       EMBL; AE000291; AAC75061.1; ALT_INIT.
EMBL; D90838; BAA15825.1; ALT_INIT.
EMBL; D90839; BAA15832.1; ALT_INIT.
EMBL; U24429; AAB47869.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A -> V
C -> S
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QGT ->
                                                    MEDLINE=97257509; PubMed=9103983;
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1025
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Outer membrane; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
1039 AA;
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Best Local Similarity
Matches 149; Conserv
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497
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61 PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120

--GE----TVNGG--TLANHDNOIVFGTTNG 82

59 P-

DP Qy DP ¢,

:| ||::|| |: || || || || || || :: | LNTCYRLVWNHMTGAFVVASELARARGKRGGVAVALSLAAVTSLPVLAA-----DIVVH 58

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121 NINDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVH 180
                                      134
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                                                                                LNGIGSTL----TDTLLNTG-----ATTNVTNDNVTDDEKKRAASVKDVLNAGWNI
                                                                                                                                                                                                   177 --VKPGTVATDTV--VNTGAEGGPDAENGDTGQFVRGDAVRTTIN----KNGRQIVRAEG
                                                                                                                                                                                                                                                -AKTSVIKEKDGKLVTGKGKDE--NGSSTDEGEGLVTAKEVIDAVNKAGWRM-----K
                                                                                                                                                                                                                                                                                    229 TANTIVVYAGGDQTVHGHALDTTLNGGYQYVHNG-GTASDTV--VNSDGWQIVKNGGVAG
                                                                                                                                                                                                                                                                                                                               328 TTTANGQTGQADKFETVTSGTNVTFASG----KGTTATVSKDDQGNITVKYDVNVGDALN
                                                                                                                                                                                                                                                                                                                                                                                                              384 VNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 SMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 GAA-----VSGTRSDGKAFSIG-GGQADALMLEKGSSFTLNAGDTATDTTVNGGLF
                                                                                                                                                                 KGVKPGTTASDNVDFVRT-------YDTVEFLSADTKTTTVNVESKDNGKKTEVKIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pIB6.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             504 GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYL--PGKSMMAIGGDT---
                                                                                                                                                                                                                                                                                                                                                                     286 NTTVN-QKGRL-QVDAGGTATNVTLKQGGALVTSTAATVT-----
                                                                                                                       135 SAGGGOSLOGRAVNTTLNGGEOWMHEGAIATGTVINDK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 29, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 RGEAGYAIGYSSISDGGNWIIKGTASGN 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    442 TARGGTLAGTTTLNNGAILTLSGKTVNN 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF STRAIN=2787 (0126:H27); MEDLINE=92326638; PubMed=1625582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adhesin aidA-I precursor
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NCBI_TaxID=562;
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31;
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                                                                                                                                                                                                                                                                                                                                                                                             106 -LKAGDNLKIKON---TNENTNDSSFTYSLKKD---LTDLTSVETEKLSFGANGNKVNIT 158
                                                                                                                                                                                                                                                                                                                                                                                                                350 HIRNGGIASGTIVNQSGY------VNISSGGYAESTIINSGGTLRVLSDGYA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGKLVTGKGKD--ENGS----- 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 RGTILNNSGRENVSNGGVSYNAMINTGGNQYIYSDGEATAAIVNTSGFQRINSGGTAPVQ 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   814 ADLSFGTAKLLSATVNGSLVNNKNIILNPTKESAGNTLTVSNYTGTPGSVISLGGVLEGD 873
                                                                                                                                                                                                                                                                                                                                   ---DSNWAVYFDEKRVLKAGAIT--- 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 -VKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKE--K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          389 NSGWNLDSKAVAGSSGKVI--SGNVSPSKGKMDETVNINAGN---NIEITRNGKNIDIAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- DVTNVAQLKGVAQN----LNNRIDNVDGNARAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         756 NVKNGGIIFDSAVVNADMAVNQNAYINISDQATINGSVNNNGSIVINNSI--INGNITND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 IAQAIATAGLVQAYLPGKSM------MAIGGDT----YRGEAGYAIGYSSISDGG
                                                                                                                                                                                                                                         1 MNKAYSIIWSHSRQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFAVNISGTVSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 RLNAFAGNVVGTILNQEGRQYVYSGATATSTVGNNEGREYVLSGGITDGTVLNSGGLQAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 -----VGSKDTNKPVRITNVAP-----
                                                                                                                                                                               Matches 156; Conservative 106; Mismatches 291; Indels 364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATTNVTNDNVTDDEKKRAASVKDVLNAG----WNIKG------
                                                                                                                                               Length 1286;
                                                                                                1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
                                                                                                                                                                                                                                                                       52 TDDDDLYLEPVQRTAVVLSFRSDKEGTGEKEGTE------
                                                                                                                                                 Score 230; DB 1;
Pred. No. 0.00027;
            EMBL; X65022; CAA46156.1; -.
PIR; S28634; S28634.
Cell adhesion; Signal; Outer membrane; Plasmid.
                                                                      ADHESIN AIDA-I.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE OF 595-1325 FROM N.A.
Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
"An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and MOM38.";
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STRAIN=K1Z / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Dayis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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-!- SIMILARITY: TO E.COLI YFAL.
-!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
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Escherichia.
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                                              YDEK_ECOLI STANDARD; PRT; 1325 AA. 932051; P76140; P77180; P77
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EcoGene; EG11780; ydeK.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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EMBL; D90794; BAA15197.1; ALT_INIT.
EMBL; X73295; CAA51730.1; ALT_FRAME.
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HYPOTHETICAL LIPOPROTEIN YDEK.
N -ACYL DIGLYCERIDE (POTENTIAL).
N -> K (IN REF. 3).
M -> S (IN REF. 3).
Mw; 26A3A066FA19AD7D CRC64;
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Hypothetical protein; Membrane; Lipoprotein; Signal;
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01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
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                                                                                                                                                                                                                                              hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION WITH THE ERYTHROCYTE MEMBRANE. SHLA SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                   FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232 PGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKD-NGKKT----EVKIGAKTSVIKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --TSSSHKADNSYQSSTASELKSDTNLTLVSHKDADVIGSQVASGGELSVESKTGNINVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       792 YTGGIDKLGSGVEAGYENNKTQAQSSKAITSGSDVKGNLT----INARDKLTQQGAQHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EG--TGEKEGTEDSNWAVYFDEKRVLKA-----GAITLKAGDNLKIK-----QNTNEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TNDSSFTYSLKKDLTDLTSVETEKLSFGANG---NKVNITSDTKGLNFAKETAGTNGDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 VHLNG-IGSTLTDTLL--NTGATTNVTNDNVTDDEKKRAASVKDVLNA----GWNIKGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :| || : | | || SSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGNKVSFLAADDKTASNTEQTKIGGGFY
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208;
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165078 MW; D669B476FE7DAD51 CRC64;
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22.3%; Pred. No. 0.013;
tive 85; Mismatches 269;
                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
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                                                                                                                                                                                                                 Poole K., Schiebel E., Braun V.; "Molecular characterization of the
                                                                                                                                                                                                                                                                                                            Bacteriol. 170:3177-3188(1988).
                                                                                                                                                                                   MEDLINE=88257037; PubMed=3290200;
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Matches 161; Conserv
                                                          NCBI_TaxID=615;
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                                                                                        958 VRDQGTQYQASKG-AVNLTADSHRSEAAANRQDEQSRDTR-----GSAG-VRVYTTTG 1008
                                                                                                                        541
848 GGAYQENAAGVDHLAAADTASTTTTKTD--VGVNIGANVDYSAVTRPVERAVGKAAKLDA 905
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                                                                                                                                                                                                                                                                                                                                                                                       Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.; "A protective protein antigen of Rickettsia rickettsii has tandemly
                                                                                                                                                                                                                                      01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kba antigen) (Cell surface
                                                                                                                                                                                                                                                                                                                                                                                            492 KEGDVTNVAQLKGVAQNLN------NRIDNVDGNARAGIAQAIATAGLVQAYLPGK
                             ---ALNVGSKDTNKPVRITNVAPGV
                                              906 TGVINDIGGIGAPNVGLDIGAQGGSSEKRSSSSQAVVSSVQAGSIDIN-----AKGE
                                                                                                            SMMAIGGDTYRGEAGYAIGYSSIS-----DGGNW-----IIKGTASGNSRGHFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
OUTER MEMBRANE PROTEIN A.
13 X APPROXIMATE TANDEM REPEATS.
A (TYPE I).
B (TYPE II).
C (TYPE II).
E (TYPE II).
F (TYPE II).
F (TYPE II).
G (TYPE II).
I (TYPE I).
I (TYPE I).
                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Cell wall; S-layer; Glycoprotein.
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InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
Antigen; Repeat; Signal; Cell wall
SIGNAL
                            452 VSL----GAGADAPTLSVDDEG----
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90354033; PubMed=2117568;
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                                                                                                                                                                                                                        STANDARD;
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286
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P15921;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1240 ASHLTIGTVAEINIGAGNLFTIDASVGDVTILN-----AQNINFRARDSVLVLSNLTG-- 1292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          891 ATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAIDNTTGGDNVGVLNLNGALSQVTGDI 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 ADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVKYDVNVGDAL------NVN- 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  386 ------QLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257 KTT----TVNVESKD---NG---KKTEVKIGAKTSVIKEKDGKLVTG----KGKDENGSS 302
                                                                                                                                                                                                                                                                                                                                                                730 ALATVNVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAIDNTTGGDNVGVLNL 789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       790 NGALSQVTGDIGNTNSLATISVGAGTATLGGAV-IKATTTKLTNAASVL----TLTNAN
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                                                                                                                                                                                                                                                                                                                30 ASATV-ATAVLATLLFATVQANATD-DDDLYLEPVQRTAVVLSFRSDKEGTGEKEGTEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 NVTNDNV---TDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDTLLNTGATT
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Escherichia.
                                                                                                                                                                                                                                                               161;
                                                                                                                                                                                                               Length 2249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  521 RAGIAQAIATAGLVQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTA
J (TYPE I).

K (TYPE II).

L (TYPE II).

M (TYPE II).

TYPE I (INCOMPLETE).

TYPE I (ANDERTE).
                                                                                                                                                                                                          6.5%; Score 197.5; DB 1;
23.0%; Pred. No. 0.02;
iive 72; Mismatches 272;
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1021
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8; 224333 N
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  875 949
950 1021
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1166 1180
2249 AA; 2
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STRAIN=K12 / MG1655;
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                                                                                                                                                                                                               Query Match
Best Local Simil
Matches 151; (
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Q53047;
               213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                       Kasai H., Rashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makinoto K., Kimura S., Kitakawa M., Kitagawa M.,
Makinoto K., Mizobuchi K., Mori H., Mori T., Motomura K.,
Makade S., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N.,
Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
Takemoto K., Takeuchi Y., Wamamoto Y., Horiuchi T.,
Takemoto K., Takeuchi Y., Wamamoto Y., Horiuchi T.,
Takepto DNA sequence of the Escherichia coli K.12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KRVLKAGAITLK-----AGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETEK 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 NNDVILDKTEKTLTIRDSVFTYTENADGT---ISLQDSNGRKATINLWQI--DEANNTVA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDDLYLEPVQRTAV-----VLSFRSDKEGTGEKEGTEDSN------WAVYFDE----- 95
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-:- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
          Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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                                                                                                                                                                                                                                                                                                                                                    Moszer I., Glaser P., Danchin A.; "Multiple IS insertion sequences near the replication terminus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 0.042;
98; Mismatches 245; Indels 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 2003;
                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B83A12C8B53220EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I -> V (IN REF. 2).
I -> V (IN REF. 2).
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0.042;
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EMBL; D8000237; AAC74487.1; ALT_SEQ.
EMBL; D90778; BAA18009.1; ALT_SEQ.
EMBL; D90778; BAA18880.1; ALT_SEQ.
EMBL; X62680; -; NOT_ANNOTATED_CDS.
ECOGENE; EG11307; ydbA.
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                                                                                                                                           MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                                                                       MEDLINE=92190338; -PubMed=1665988;
MEDLINE=97426617; PubMed=9278503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       205949 MW;
                                                                                                                                                                                                                                                                                                          SEQUENCE OF 464-2003 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli K-12.";
Biochimie 73:1361-1374(1991).
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Best Local Similarity 20.7%
Matches 143; Conservative
                                                                                                                                                                                                                                                                               DNA Res. 3:363-377(1996).
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                                                                                                               SEQUENCE FROM N.A.
                                                        Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                          STRAIN=K12
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                                                        Mau B.,
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30-MAY-2000 (Rel. 39, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
00-uter membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90136087; PubMed=2515418; Gilmore R.D. Jr., Joste N., McDonald G.A.; Cloning, expression and sequence analysis of the gene encoding the 120 kD surface-exposed protein of Rickettsia rickettsii."; Mol. Microbiol. 3:1579-1586(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
SUBCELLULAR LOCATION: CELL WALL, THIS BACTERIUM IS COVERED BY LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                    493 QAIVNNEG---ESTITNGGTGTQINGNDATANNSGKTTVDGKDSTGTKIAGNIGIVNLDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLTVTGGAHGVENIGDNGTVNNKGDIVVSDTGSIGVLINGEGATVSNTGDVNVSNEATGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RAASVKDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKK-
                                                                           377 GTMTVTDPESIGIQVDG-DQAVVNNEGESAITNGGTGTQINGDDATANNNGKTTVDGKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DOGNITVKYDVNVGDALNVNQL------QNSG-WNLDSKA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             457 GADAPTLSV---------DDEGALNVGSKDTNKPVRITNVAPGVKEGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor."; Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                               --TEVKIGAKTSVIKEKDGKLVT---GKGKDENG-SSTDEGEGLVTAKE-----VIDA-
                                                                                                                                                                                                                                                                                                                                            ---VNKAGWRMKTTTANGQTG-QADKFETVTSGTNVTFASGKGTTAT----VSKD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 SGDANTVNITGNVLVDKDKTADNAAEYFFDPSVGINVYGSDNN--VTLDGKLTVVSDSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNVAQ--LKGVAQNLNNRIDNVDGNA------RAGIAQAIATAGLVQAY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1654 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 DEKRVLKAGAITLKAGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGN 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 GNLAAQIKVPNAITLTGNFTGDASNPGNTAG-----VITFDANGTLESASADANVAVTNN 457
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             15 AWVVVSELTRNHTKRA-----SATVATAVLATL-------LFATVQA-NATDDD 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56 DLYLEPVQRTAVVLSFR-----SDKEGTGEK-------EGTEDSNWAVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 EFNTVAVDGQLTANAGAANAVIGTNNGAGRAAGFVVSVD-------NGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 KVNITSDTKGLNFAKETAGTNGDPTV-HLNGIGSTLTDTLLNTGATTNVTNDN--VTDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 ---VESKDNG------KKTEVKIGAKTSVIKEKDGKLVTGK-----GKDENGSSTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 ITAIEASGAGVVQLSGTHAAELRLGNAGSIFKLADGTVINGKVNQTALVGGALAAGTITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT-SGTNVTFASG-----K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518 DGSATITGD--IGNAGGAAALQRITLAN-----DAKKTLTLGGANIIGAGGGTIDLQAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTATVSKDDQGNITVKYDVNVG-DALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKMDETV-NINAGNNIEITRNG----KNIDIATSMAPQF----SSVSLGAGA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 GANNKTLGOFNIGSSKTVLSNGNVAINELVIGNDGAVQFAHDTYLITRTTNAAGQGKIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----DAPTLSVDDEGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  679 NPVVNNGTTLA----AGTNLGSA-TNPLAEINFGSKGVNVDTVLNVGE--GVNLYATN-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNVDGNARAGIAQAIAT---AGLV------QAYLPGKSMMAIGGDTYRGEAGYAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 VATIDGQVYAKDMVIQSANATGQVNFRHIVDVGADGTTAFKTAASKVTITQDSNFGNTDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            570 GGTIKLT-STONNIVVDFDLAIATDOTGV-----VDASSLTNAOTLTINGKIG-TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211 KKRAASVK - DVLNAGWNIKG - - VKPGTTASDNVDFVRTYD - - - TVEFLSADTKTTTVN -
                                                                                                                                                                                                                                                                                                                                                                                                       Indels 165;
                                                                                                                                                                                                                                                                                                                                                                     Length 1654;
                                                                                                                                                                                                                                                 120 KDA SURFACE-EXPOSED PROTEIN. 32 KDA BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                         D7AB70FB7087F618 CRC64;
                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                     284;
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85; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                 Score 189.5;
                                                                                                                                                                                                                                                                                         POLY - THR
                                                                                                                                                                   EMBL; X16353; CAA34403.1; -.
InterPro: PPRO3788; rompA_rompB.
Pfam; PF02708; rompA_rompB; 1.
Antigen; S-layer; Cell wall:
                                                                                                                                                                                                                                                                                                         1654 AA; 168184 MW;
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                                                                                                                                                                                                                                                                                                                                                                                     21.78;
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Matches 148; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group."; submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-! FUNCTION: THE 120 KDA SURRACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY A S-
          099KAX3; O9KK98; O9KX45;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen) (Sor5) (romps)
(romp B) [Contains: 120 kDa surface-exposed protein (Surface protein)
antigen) (120 kDa outer membrane protein omps); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 KDA SURPAGE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
P -> A (IN STRAIN INDIAN TICK TYPHUS).
G -> S (IN STRAIN INDIAN TICK TYPHUS).
K -> N (IN STRAIN INDIAN TICK TYPHUS).
V -> A (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
N -> T (IN STRAIN INDIAN TICK TYPHUS).
A -> T (IN STRAIN INDIAN TICK TYPHUS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
-!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                         "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roux V., Raoult D.; "Phylogenetic analysis of members of the genus Rickettsia using the
                                                                                                                                                                                                                                                                                                                                                Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                    Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene coding the outer-membrane protein rOmpB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AF149110; AAD39533.1; -. InterPro; IPR003859; rOmpA_rOmpB. Pfan; PF02708; rOmpA_rOmpB; 1. Antigen; S-layer; Cell wall; Complete proteome. CHAIN
1655 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Indian tick typhus, and Malish 7;
MEDLINE=20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                              MEDLINE-21442074; PubMed-11557893;
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STANDARD;
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                                                                                                                                                                 211 NGTLN------VTNGFIKVSSKSFATVNVINIGDGQGIMFNTDADNVNTLNLQANGATI 263
                                                                                                                                                                                                                                        116 ONTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG 175
                                                                                                                                                                                                                                                                                                                                                                           KIGAKTSVIKEKDGKLVTGK-----GKDENGSSTDEGEGLVTAKEVIDAVNKAGWRM 326
                                                                                                                                                                                                                                                                                                                                                                                            FIGNAGSVFKLADGTVINGKVNQTALVGGALAAGTITLDGSATITG----DIGNAGG--- 532
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                                                                                                                                                                                                                  264 TF-NGTDGTGRLVLLSKNAAATDFNVTGSLGGNLKGIIEFNTVAVNGQLKANAGANAAVI 322
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                                                                                                                                                                                                                                                                                                        365 QVNFRHIVDVGTDGTTAFKTAASKVAITQNSNFGTTDFGNLAAQIIVPNTMTLNGNFTGD 424
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                                                                                                                                                10 NSALNAWVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLEPVQRTAVVL 69
  STRAIN INDIAN TICK TYPHUS)
                                                                                                                                                                                              ----EKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIK
                                                                                                                                                                                                                                                                                    176 DPT----VHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKD----VLNAGWNIK
                                                                                                                                                                                                                                                                                                                                GVKPGTTASDNVDFVRTYD---TVEFLSADTKTTTVN----VESKDNG-----KKTEV
                                                                                                                                                                                                                                                                                                                                                     425 ASNPGNTAG-----VITFDANGTLASASADANVAVTNNITAIEASGAGVVQLSGTHAAEL
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                                                                                                      Length 1655;
R -> L (IN STRAIN INDIAN TICK
KD -> GH (IN REF. 3).
F -> S (IN REF. 3).
E -> D (IN REF. 3).
G -> S (IN REF. 3).
G -> S (IN REF. 3).
H -> R (IN REF. 3).
MW; E49E19377D5FCE37 CRC64;
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                                                                                                     DB 1;
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(Rel. 16, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                    Score 188.5; DB
Pred. No. 0.039;
; Mismatches 2
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Similarity 22.3%; Pre
                                                                   AA; 168342
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SEQUENCE FROM N.A.
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANDOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE. SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIDNVDGNARAGIAQAIATA-GLVQAYLPGKSMMAIGGDTYRGEAGY----AIGYSSISD
                                                                                                              Xanthomonas campestris pv. translucens.";
Mol. Gen. Genet. 223:163-166(1990).

-!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CRYSTALLIZATION IN SUPERCOOLED WATER.
-!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
OCTAPEPETIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAGADSTLIAGYGSTQTAGSDSSLTAGYG-----STQTARQGSDITAGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VIAGYGSTG-----TAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTARKGSDMTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 AKTSVIKEKDGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAG------DNLKIK--QNTNENTNDSSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAGYGSTQTARKGSDITAGYGSTGTAGADSTLIAGYGSTQTSGSDSSLTAGYGSTQTARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----TAGTNGDPTVHLNGIGSTLT---DTLLNTGATTNVTNDNVTDDEKKRAASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDVLNAGWNIKGVKPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGYGSTGTAGADSTLIAGYGSTQTAGSD--SSLTAGY----GSTQTARQGSDVTAGYGST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1567;
                                                                         "Conserved repetition in the ice nucleation gene inax from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             855 GSDVTAGYGSTGTAGADSTLISGYGSTQTAGSDSSLTAGYGSTQTARKGSD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ice nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.2%; Score 188; DB 1;
20.3%; Pred. No. 0.039;
ive 82; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00818; ICe_nucleation; 81.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYSLKKDLT - - - - DLTSVETEKLSFGA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000258; Ice_nucleatn
    PubMed=2259339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X52970; CAA37140.1; -.
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HSSP; P06620; 11NA.
                                        Orser C.S.
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Best Local Similarity
Matches 117; Conserv
MEDLINE-91080859;
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Crocquet-Valdes P.A., Weiss K., Walker D.H.; "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain)."; Gene 140:115-119(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGDPTVHLN-----GIGSTLTDT 191
                                                                                                                                    DTVEFLSAD-----TKTTTVNVESKDNGKKTEVKIGAKTSVIKEKD----GKLVTGKG 295
                                                                                                                                                                                                                                                                        DKFETVTSGTNVTFASGKGTTATVS--KDDQGNITVKYDVNVGDALNVNQLQNSGWNLDS 396
                                                                                                                                                                                                                                                                                                                                                                         TISGGFS---YTGGVDKVGSKADFQYDKQHTQTEVTKNRGSQTEVAGDLTITANKDLLHE 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OMPA_RICCN STANDARD; PRT; 2021 AA.
052657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669; Q52670; Q52670; Q52674;
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VR-----ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQ
                                                                                                                                                           KLGIHSLGDINVKSAQQVTKIDDEKTSLAITGHAKEVEDKQYSAGFHITHTTNKNTSTET
                                                                                                                                                                                                                                                                                                                                                                                                                                  483 AQGSITAQGAKLHANENVLVNAKDNINLNVQK----TNNDKTVTDNHVMWGGIGGGQNKN
                                                                   LLINTGATTINVINDINVIDDEKKRAASVKDVLNAGWNIKG-----VKPGTTASDNVDFVRTY
                                                                                        K-----DENGSST-----DEGEGLVT---AKEVIDAVNKAGWRMKTTTANGQTGQA
                                                                                                                                                                                                                                                                                            397 KAVAGSSGKVISGNVSPSKGKMD------ETVNINAGNNIEIT-------
                                                                                                                                                                                                                                                                                                                                                                                                            --RNGKNID-IATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan;
MEDLINE-97015921; PubMed-8862558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94171067; PubMed=8125327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 8-204 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antigen) (rOmpA) (rOmp A).
OMPA OR RC1273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rickettsia conorii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30;
FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM BERTHROCYTES METHORYTES HEME-IRON BERTHROCYTES METHORYTES HEMB FUNCTION: WITH THE ERYTHROCYTE MEMBRANE. HEMA SUBCELLULAR LOCATION: Outer membrane.

MISCELLANDOUS: THE CONSENDE AMPHRATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.

SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 LTKTELKGKNITLVAS-----SHNQIKASDLMGDDITLQGADLTI-----DGKQLQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----AITLKAGDNL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 KI------KONTNENTNDSSFTYSLKK------DLTDLT----- 139
                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ISOLATE 477-12;
MEDLINE-90170827; PubMed-2407716;
MEDLINE-90170827; PubMed-2407716;
MEDLINE-90170827; PubMed-2407716;
MUPHOFI T.S., Welch R.A.;
"Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpmA and hpmB) reveals sequence similarity with the Serratia marcescens hemolysin genes (shlA and shlB).";
J. Bacteriol. 172:1206-1216(1990).
I. FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 184; DB 1; Length 1577;
21.5%; Pred. No. 0.062;
tive 80; Mismatches 253; Indels 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HEMOLYSIN. IN 5975E0C924B2D9 CRC64;
                                                                          1220 AGYKSTLTAGYGSNSTAGHESSLIAGYGSTQIAGYE 1255
                                                                                                                                                                                                   01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                     1577 AA
                                                 GG--NWIIKGTASGNSRGH-----FGASASVGYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKEGTEDSNW-----AVYFDEKRVLKAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165869 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M30186; AAA25657.1; -.
PIR; A35140; A35140.
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                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                        Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1577 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                        Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=584;
                                                                                                                                                                    HLYA_PROMI
P16466;
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                                                                                                                                  RESULT 10
HLYA_PROMI
                                                 267
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Barbe V.,

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CONFLICT
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N -> NN (IN STRAIN INDIAN TICK TYPHUS).

N -> NN (IN STRAIN INDIAN TICK TYPHUS).

MISSING (IN STRAIN M1).

MISSING (IN STRAIN M0ROCCAN).

VT -> II (IN STRAIN INDIAN TICK TYPHUS).

D -> A (IN STRAINS INDIAN TICK TYPHUS).
Roux V., Fournier P.E., Raoult D.; "Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rompa."; J. Clin. Microbiol. 34:2058-2065(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M -> H (IN STRAIN MOROCCAN).
M -> I (IN STRAIN INDIAN TICK TYPHUS).
Q -> K (IN REF. 1).
I -> V (IN REF. 1).
V -> I (IN REF. 1).
G -> D (IN REF. 1).
I -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IS -> VN (IN REF. 1).
KATLGGAIIKATTTK -> LLQVQGGVVKANTIN (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VN -> IS (IN REF. 1).
LLRVQGGVVKSNTIN -> KATLGGAIIKATTTK (IN
                                                                                                              study
                                                                                                                                                            BY
                                                                                STRAIN-Indian tick typins, M., Malish 7, and Moroccan;
Raoult D., Fournier P.E., Roux V.;
Phylogenetic analysis of spotted fever group rickettsiae by st
of the outer surface protein rompa.";
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
-: FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).
-: SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED.
S-LAYER WITH HEXAGONAL SYMMETRY.
-: PTW. GLYCOSYLARDE (BY SIMILARITY).
-: SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OUTER MEMBRANE PROTEIN A.
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N -> D (IN REF. 1).

V -> I (IN REF. 1).

N -> D (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                      SEQUENCE OF 953-2012 FROM N.A.
                                                                                                                                                                                                                                                                                                                                          . 043794, AAB49549.1;
. 043798, AAB49550.1;
. 045244, AAB49551.1;
. 046218, AAB4956.1;
. 046918, AAB6663.1;
. 083440, AAC35179.1;
. 083443, AAC35179.1;
                                                                                                                                                                                                                                                                                                                   EMBL; U01028; AAA17405.1; -. EMBL; AE008674; AAL03811.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 QRTAV-----VLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAI----TLKA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 VVTGAIDNTGNANNGIVTFTGDSTVTG-NIGNTNALATISVGAGKATLGGAIIKATTTKL 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GDNLKIKQNTNE-----LISVETEKLSF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NGNKVNITSDTKGLNFAKETAGTN-----GDPTVHLNGIGSTLT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             287 DGKLVTG----KGKDENGSSTDEGEGLVTAK----EVIDAVNKA-----GWRMKTTTA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----GQTGQADK-----FETVT---SGTN----VTFASGKG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 T-----TATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISG 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                  10 NSALNAWVVVSELTRN-HTKRASATVAT-AVLATLLFATVQANATDDDD-----LYLEPV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             534 IDNASAVTFINPVVVTGAIDNTGNANNGIVTFTGDSTVTGNIGNTNALATISVGAGKATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594 GGAIIKATTTKLTDNASAVTFTNPVVVTGAIDNTGNANNGIVTFTGNSTVTGN-IGNTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 DTLLNTGA------TTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 SDNVDFVRTYDTVEFLSADTKTT----TVNV---ESKDNG---KKTEVKIGAKTSVIKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 703 VDNVGVLNLNGALSQVTGNIGNTNALATISVGAGKATLGGAVIKATTTKLTDNASAVTFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433 TRNGKN--IDIATSMAPQF-----SSVSLGAG-----ADAPTLSVDD-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         469 GAL---NVGSKDTNKPVRITN-VAPGVKEGDV------TNVAQLKGVAQNLNN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---RIDNVDGNARAGIAQAIA-TAGLVQAYLPGKSMMAIG
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                                                                                                                                                                                                                                                                                                               6.0%; Score 182; DB 1; Length 2021;
21.1%; Pred. No. 0.1;
Live 88; Mismatches 278; Indels 280;
K -> Q (IN REF. 1).
N -> Y (IN REF. 4).
H -> N (IN REF. 1).
G -> D (IN REF. 1).
E -> G (IN REF. 1).
A -> V (IN REF. 1).
A -> V (IN REF. 1).
A -> P (IN REF. 1).
E -> LP (IN REF. 1).
MS -> LP (IN REF. 1).
E -> A (IN REF. 1).
MTAPLP -> ITPPLS (IN REF. 1).
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nes 173; Conserv
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Length 1645;

DB 1;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a licensee agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

"Evidence for proteolytic cleavage of the 120-kilodalton outer
membrane protein of rickettsiae: identification of an avirulent
processing.";

Infect. Immun. 60:159-165(1992).

-! FUNCTION: THE 120 KDA SURRACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
-! FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
-SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL. SYMMETRY.
-! SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                        (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB) (rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
                                                                                                                                                                                                                                                                                                                     STRAIN=WILMINGTON;
MEDLINE=94040787; PubMed=8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 40, Last annotation update)
16-CCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  binding sites on CNBr fragments of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 KDA SURFACE-EXPOSED PROTEIN. 32 KDA BETA PEPTIDE.
                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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12 V -> I (IN REF. 2).

13 G -> A (IN REF. 2).

16 G -> S (IN REF. 2).

169698 MW; OCB5641C7EB185EE CRC64;
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                                    1645 AA.
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                                  PRT;
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InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WILMINGTON;
MEDLINE-92114896; PubMed-1370573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=92104668; PubMed-1729180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody be the S-layer protein antigens of F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION OF CLEAVAGE SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Immunol. 29:95-105(1992)
                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGAGA---DAPTLSVDD--EGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQN 508
                                                                                                                                                                                                                                                                                                                                                                                                                                   NIGD - NOGLMFNTTPDAANALNLQGGGNTINFNGRDGTGKLVLVSKNGNATEFNVTGSL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 GGNLKGVIEFDTTAAAGKLIANGGAANAVIGTDNGAGRAAGFIVSVDNGNAATISGQVYA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-----KGKMDETVNI-------NAGNNIEITRNGKNIDIATSMAPQFSSVS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 LNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMA-IGGDTYRGEAGYAIGYSSISDG 567
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                                                                                                                                                        66 AVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNENTNDS 125
                                                                                                                  10 KIISAGLVTASTATIVAGFSGVAMGAVMQYNRTTNAAATTVDGAGFDQTGAGVNLPVATN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                 176 DPTVHLNGIGSTLTDTLLNTGATTNVTND-----NVTDDEKKRAASVKDVLNAGWNIKGV
                                                                                                                                                                                                                                                                                                                                       --VLEFNLINPTTQEAPLTLGDNAKIVNGANGILNITNGFVK----VSDKTFAG--IKTI
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                                                                                                                                                                                               SVITANSNNAITFNTPNGNLNS---LFLDTANTL---AVTINENTTLGFVTNVTKQGNFF
                                                                                                                                                                                                                                      126 SFTYSLKKDLT----DLTSVETEKLSFGAN-GNKVNI----TSDTKGLNFAKETAGTNG
                                                                                                                                                                                                                                                                          124 NFTIGAGKSLTITGHGITAQQAATTKSAQNVVSKVNAGAAINDNDLSGVGSIDFTAAPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---STDEG-----EGLVTA
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                                                                                                                                                                                                                                                                                                                                                                                              231 KPGTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKD------NGKKTEVKI----
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Blaser M.J., Gotschlich E.C.;
"Surface array protein of Campylobacter fetus. Cloning and gene
                                        Indels
                                                                             28 KRASATVATAVLATLLFA-------TVQANATDDDDLYLE---
                                        90; Mismatches 265;
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(Rel. 29, Last sequence update)
(Rel. 30, Last annotation update)
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  Score 180.5; DB Pred. No. 0.097;
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SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
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Query Match
Best Local Similarity 21.1<sup>§</sup>
Matches 145; Conservative
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                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                             Blaser M.J., Gotschlich E.C.;
J. Balol. Chem. 265:19372-19372 (1990).
-!- FUNCTION: THE S.LAYER IS A PARGRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                             CRITICAL FOR VIRULENCE.
SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY
S-LAYER WITH HEXAGONAL SYMMETRY.
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SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;
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(2.9%; Pred. No. 0.055;
ve 89; Mismatches 251;
Biol. Chem. 265:14529-14535(1990)
                                                            MEDLINE=91035477; PubMed=2229082;
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Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gilmore R.D. Jr., Joste N., McDonald G.A.;

120 kD surface-exposed protein of Rickettsia rickettsii.";

Mol. Microbiol. 3:1579-1586(1989).

-!- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS

RICKETTSIA. VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-!- SUBCELLULAR LOCATION. CELL WALL. THIS BACTERIUM IS COVERED BY A
                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                          (Rel. 14, Created)
(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
1300 AA
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Antigen: Glycoprotein; Cell wall; S-layer
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N-L
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PRT;
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                                                                                                                                                                kDa surface-exposed protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X16353; CAA34402.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein;
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                                                                                                                                                                                                                                 Rickettsia rickettsii.
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(POTENTIAL)

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NKIYRIIWNSALNA-----WVVVSELTRNHTKRASATVATAVLATLLFATVQA----
             hermoanaerobacter thermosulfurogenes (Clostridium
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DOMAIN
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                                                                                                                                                                                                                                                                                                     TDQTGVVDASSLTNAQTLTINGKIGTIGANNKTLGQFNIGSSKTVLSNGNVAINELVIGN 297
                                                                             Gaps
                                                                                                                        79
                                                                                                 ASATVATAVLATLLFATVQAN--ATDDDDLYLEPVQRTAVVL--SFRSDKEGTGEKEGTE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1994 (Rel. 30, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase
type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase); Pullulanase (EC 3.2.1.1) (1,4-alpha-D-glucan
glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)]
                                                                                                                                             DSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNENTNDSSFTYSLKKDLTDLTSVETEK
                                                                                                                                                                                                                                                                                                                                                DGAVQFAHDTYLITRTTNAAGQGKIIFNPVVNNGTTLAAGTNLGSATNPLAEINFGSKGV
                                                                                                                                                                                                                                                                                                                                                                                     NVDTVLNVGECVNLYATNITTTDANVGSFVFNAGGTNIVSGTVGGQQGKKFNTVALENGT
                                                                                                                       22 ADGTTAFKTAASKVTITQDSNFGNTDFGNLAAQIKVPNAITLTGNFTGDASNPGNTAG--
                                                                                                                                                                  ----VITFDANGTLESAS----ADANVAV-----TNNITAIEASGAGVVQLSGTHAAE
                                                                                                                                                                                                             125 LRLGNAGSIFKLADGTVINGKVNOTALVGGALAAGTITLDG-SATITGDIGNAGGAAALQ
                                                                                                                                                                                                                                     NDNVTDDEKKRAASVKDVLNAGWNIKGVKPGT------TASDN---VDF---VR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGNARAGIAQAIATAGLVQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTA
                                                                                                                                                                                          LSFGANGNKVNITSDTKGLNFAKETA - - - GTNGDPTVHLNGIGSTLTDTLLNTGATTNVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSV-----DDEGALNVGSKDTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNV
                                                                           Indels 207;
                                                      Length 1300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----SMAPQFSSVSLGAGAD-
                      MW; E09E52C3F647243D CRC64;
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                                                          .5;
0.13;
- 282;
N-LINKED (POTENTIAL)
N-LINKED (POTENTIAL)
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                                                                  Pred. No. 0.13 93; Mismatches
                                                      Score 175.5;
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                                                     5.8%;
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1300 AA; 132801
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                                                                 Similarity
                                                                          Matches 153;
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                                                     Query Match
Best Local 3
 CARBOHYD
            CARBOHYD
                      SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is nor removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib-sib.ch).
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                                                                                                                                                                                                Matuschek M., Burchhardt G., Sahm K., Bahl H.;
Matuschek M., Burchhardt G., Sahm K., Bahl H.;

"Pullulanase of Thermoanaerobacterium thermosulfurigenes EMI
(Clostridium thermosulfurogenes): molecular analysis of the gene,
composite structure of the enzyme, and a common model for its
attachment to the cell surface.";
J. Bacteriol. 176:3295-3302(1994).

C. CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
inkages in oligosaccharides and polysaccharides.

C. CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
linkages in pullulan and in amylopectin and glycogen, and the
alpha-and beta-limit dextrins of amylopectin and glycogen.

S-LAYER ANCHOR.

S-LAYER ANCHOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PTM: GLYCOSYLATED.
-!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS01072; SLH_DOMAIN; 3.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB00841)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMYLOPOLLULANASE.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
BY SIMILARITY.
BY SIMILARITY.
SLH 1.
SLH 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 175.5; DB 1;
; Pred. No. 0.2;
94; Mismatches 219;
                         group;
                                                  Thermoanaerobacter group; Thermoanaerobacterium
                      Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
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Interpro; IPR004193; isoamylase_N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02806; alpha-amylase_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein
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InterPro; IPR003961; FN_III.
InterPro; IPR001119; SLH.
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                                                                                                                                                      STRAIN=DSM 3896 / EM1;
MEDLINE=94252998; PubMed=8195085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF02903; alpha-amylase_N; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF02922; isoamylase_N; 1. PF00395; SLH; 3.
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\; 206104 N
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                      Bacteria; Firmicutes;
thermosulfurogenes).
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Best Local Similarity
                                                                                                                                SEQUENCE FROM N.A.
                                                                           NCBI_TaxID=33950;
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1268 VNLAGTFPNATWDPSAQQMTKIDNNTYSITLTLD-EGTQIEYKYARGSWDKVEKDEYGNE 1326
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                                                                                                                                                       144 EKLSFGA-NGNKVNITSDT----KGLNFAKETA---GTN------GDPTVHLNGIGST 187
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                                         -----NAT-DDDDLYLEPVQRTAVVLSFRSDKEGT------GEKEGTEDSNWAVY 92
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Search completed: July 3, 2002, 08:49:07 Job time: 713 sec

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1 MNKIYRIIWNSALNAWVVVS......TASGNSRGHFGASASVGYQW 594
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Q9jpr7 neisseria m	Q9jps9 neisseria m	Q93qy2 neisseria m	Q9jps5 neisseria m	O9jphO neisseria m	O9jpi0 neisseria m		Q9jqw4 neisseria m	Q9jps4 neisseria m	Q9jps1 neisseria m	P71401 haemophilus		Q9f3x6 pasteurella	Q9pd50 xylella fas	xylella	Q9f2d8 salmonella	pasteur	Q9pd63 xylella fas	Q92kq7 rhizobium m	Q98hj2 rhizobium l	Q93ty6 staphylococ	Q916t7 escherichia	Q9fda0 xanthomonas	Q916t8 escherichia	Q9xd84 escherichia	Q9al50 shigella fl		f03 shigella	Q9rni2 haemophilus
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17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

1	Q9JPH7 PRELIMINARY; PRT; 594 AA. Q9JPH7;	01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	ANE PROTEIN C	Neisseria meningitidis. Bacteria: Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	NCB1_10X1D-40/; [1]	SEQUENCE FROM N.A. STRAINE BE1198, AND 297-0; MEDITANE-20175756. DINAMAGA 10710308.	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M. Hundt R., Knaph R., Rlair E., Mason T., Tettelin H.,	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,	Moxon E.R., Grandi G., Rappuoli R.; "Identification of Vaccine Candidates Against Serogroup B	Meningococcus by Whole-Genome Sequencing.";	2]	SEQUENCE FROM N.A.	SIRAIN-BZ198; Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;	"Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.":	Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL: AF226368: AAF42517.1:	EMBL; AF226358; AAF42507.1;	COUENCE 594 AA; 62361 MW; 436BDDED68263C5C CRC64;
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592:
                  Query Match
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MEDLINE=20175756; Pubmed=10710308; Giuliani M.M., Arico' B., MEDLINE=20175756; Pubmed=10710308; Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Hood D.M., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R., "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                               LNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTASDNV
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Length 594;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
100.0%; Score 3023; DB 2; 100.0%; Pred. No. 1.1e-118;
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          Similarity
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NCBI_TaxID=487;
                  Matches 594;
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"Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing.";
                                                                                                         MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE
                                                                                                                                                                     PVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ----
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0EC-2001 (TrEMBLrel. 19, Last annotation update)
00TER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
                                          Indels
  Length
Score 2997; DB 2;
Pred. No. 1.3e-117;
                                          0: Mismatches
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MEDLINE=20175756; PubMed=10710308;
99.1%;
99.0%;
                                          Conservative
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Neisseria meningitidis.
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Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comeduci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Moxon E.R., Grandi G., Rapuders N.J., Granoff D.M., Venter C., "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."; Science 287.1816-1820(2000).

EMBL: AF226359; AAR425081: -. SEQUENCE 598 AA; 62763 MM; 63A6A3BD7F0F2EE3 CRC64;
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Best Local Simi]
Matches 583; (
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NCBI_TaxID=487;
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                               Jennings M.P.
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               STRAIN-H15;
STRAIN-H15;
Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jenning, "Identification and characterization of a gene encoding; membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226381; AAF425301;
EMBL; AF25607; AAF686881;
SEOUENCE 598 AA; 62763 MW; E6C7AEF0BB8A63CB CRC64;
                                                                                                                        Length
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                                                                                                                       Score 2971; DB 2;
Pred. No. 1.6e-116;
1; Mismatches 7;
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MEDLINE=20175756; PubMed=10710308;
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98.0%;
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                                                                                                                        Query Match 98.3
Best Local Similarity 98.0
Matches 586; Conservative
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Neisseria meningitidis
           SEQUENCE FROM N.A.
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01-MAR-2001 (
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  Length 598;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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Score 2957; DB 2;
Pred. No. 6.2e-116;
2; Mismatches 9;
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97.8%;
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       Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
"Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF157603, AAK68864 1. .
SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;
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                                                                                                                                                                                                                                                                                 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK 296
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STRAIN=NGB31;
MEDLINE-20175556; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                   Score 2948; DB 2;
Pred. No. 1.5e-115;
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97.3%;
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Best Local Similarity 97.3
Matches 582; Conservative
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NCBI_TaxID=487;
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Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; Indentification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing."; science 287:1816-1820(2000).
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STRAIN=NG3/88, AND B2232;
MEDLINE-20175756; Pubmed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico'
                                                                                                                                                                                                                                                                                       Indels
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SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                          95.5%; Score 2888; DB 2; 96.0%; Pred. No. 4.6e-113;
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O1-OCT-2000 (TTEMBLrel. 15, La
O1-MAR-2001 (TTEMBLREL. 16, La
OUTER MEMBRANE PROTEIN GNA992.
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Matches 570; Conservative
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novel outer

oxon R., Jennings M.P.; gene encoding a novel o

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Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennin "Identification and characterization of a gene encoding membrane protein of Nelsseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI57605; AAK68666.1;
SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;
                                                                                                                     Conservative
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Best Local Simi
Matches 568;
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     Galectti C.L., Luzzi B., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettellin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B Meningococus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
Science 287:2816-1820(2011).
SEQUENCE 594 AA, 62086 MW; 1B25E03B90D04B46 CRC64;
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95.8%; Pred. No. 6.7e-113;
iive 4; Mismatches 21;
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Comanducci M., Jennings G.T., Baldi L.,
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Bacteria; Proteobacteria; beta
NCBI_TaxID=487;
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01-DEC-2001 (TrEMBLrel. 19,
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Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN)
                                                                                                 Indels
95.1%; Score 2874; DB 2; 95.6%; Pred. No. 1.7e-112;
                                                                                             5; Mismatches
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01-DEC-2001 (TrEMBLrel. 19, Last anno
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Bacteria; Proteobacteria; beta
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Mon

SEQUENCE FROM N.A.

STRAIN=H38;

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VQAYLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQ 593
              Neisseriaceae; Neisseria
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"Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFAT-----VQANATD
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                                                                                                                                                                                                                                                                                                  AF226371; AAF42520.1; -. NCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    92.6%; Score 2800; DB 2; 92.7%; Pred. No. 2.1e-109; tive 13; Mismatches 23;
              subdivision;
                                                                                                                                                                                                                                                                Meningococcus by Whole-Genome Sequencing.", Science 287:1816-1820(2000).
                                                                                                    MEDLINE=20175756; PubMed=10710308;
                beta
Neisseria meningitidis.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
ses 557; Conserv
                                                                     FROM N.A.
                                  NCBI_TaxID=487
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                                                                                       STRAIN=E26
                                                                   SEQUENCE
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Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.; Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
                                                                                                                                                                           Jennings M.P.
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                                                                                                                                                                                                                                                                                                                                         599;
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                                                                                                                                                                             Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennine "Identification and characterization of a gene encoding immembrane protein of Neisseria meningitidis.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF226083; AAF42532.1;
EMBL; AF127608, AAK68869.1;
EDBUS AR580809.1;
EDBUS AR580809.1;
EDBUS AR580809.1;
EDBUS AR580809.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GNA992.
                                                                                                                                                                                                                                                                                                                                       Query Match 92.7%; Score 2802.5; DB 2; Best Local Similarity 92.5%; Pred. No. 1.7e-109; Matches 554; Conservative 12; Mismatches 28; I
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                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                              ٠ vs
                                                                                                                            Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R., "Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                             NKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYL
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                                                                                                                                                                                                                                 (2527.1; -. 61661 MW; 8AA476AC300D80C8 CRC64;
       01-OCT-2000 (TrEMBLrel. 15, Created)
U-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992.
                                                                                                                                                                                                                                                                     Score 2782; DB 2;
Pred. No. 1.2e-108;
9; Mismatches 23;
                                                                                                                                                                                                        Meningococcus by Whole Genome Sequencing.";
Science 287:1816-1820(2000)
                                                                                                          STRAIN=NGE28;
MEDLINE=20175756; PubMed=10710308;
                                                                                                                                                                                                                                                                      92.0%;
93.3%;
                                                                                                                                                                                                                                                                                          Matches 556; Conservative
                                                                                                                                                                                                                             EMBL; AF226378; AAF42527
SEQUENCE 590 AA: 6166
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=487;
                                                 GNA992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                           Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD---DDDL 57
                                                                                                                                                                                                                                                                                                        Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon B.R., Grandi G., Rappuoli R.; Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLPGKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62113 MW; 533453CAE5A91E1F CRC64;
                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL; AF226366; AAF42515.1; -.
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591
PRT;
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MEDLINE=20175756; PubMed=10710308;
                                                                                                        OUTER MEMBRANE PROTEIN GNA992
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Best Local Similarity 92.19
Matches 551; Conservative
PRELIMINARY;
                                                                                                                                                    Neisseria meningitidis
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                                                                                                                                                                                                NCBI_TaxID=487;
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416

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KMDETVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSK 476
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                      175 TTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA
                                                                                                                                                                                         DINKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQA
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NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNGD
                                                                                                                                                                     SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTGKGK
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SEQUENCE 599 AA; 62693 M
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01-MAR-2001
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Q9JPS8
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STRAIN-MCSB / SEROGROUP B;
STRAIN-2017755; PubMed-10710307;
Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain MC58";
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                                                                                                                                                                                                                        Neisseria meningitidis, and
Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                               PEDGENCE TOWN WAS SEROCROUP B, B2169, B283, AND H44/76;
MEDLINE-20175756; PubMed=10710308;
Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Caleotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Rapp B., Blair E., Mason T., Tettelin H., Hoxon E.R., Grandi G., Sanders N.J., Granoff D.M., Venter C., Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.7%; Score 2740.5; DB 16; Length 591;
                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meningococcus by Whole-Genome Sequencing."; Science 287:1816-1820(2000).
                                                    591 AA
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Best Local Similarity 92.1%,
Matches 551; Conservative
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GNA992 OR NMB0992 OR NHHA.
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Q9JR18;
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60 EPVQRTAVVLSFRSDKEGTGEKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ--- 116
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                                                                                                                                                                                                                         Proteobacteria; beta subdivision; Neisseriaceae; Neisseria
                                                                                                                                                                                                                                                                                                                                                                                Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecchi B., Galectti C.L., Luzzi E., Monetti R., Marchetti E., Mora M., Nuti S. Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettellin H., Brood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R., "Identification of Vaccine Candidates Against Serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MNKIYRIIWNSALNAWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL
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                                                    (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
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Pred. No. 1.1e-106;
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599 AA
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  PRT;
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                                                                                                                                     OUTER MEMBRANE PROTEIN GNA992.
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LYLDPVQRTVAVLIVNSDKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
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Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
"Identification and characterisation of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125375; AAK09243.1;
SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
                                                                                                       A--SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTG 293
                                                                                                                KGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFA 353
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                                                                 DPTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTT
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Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
NCBL_TaxID=487;
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Last annotation update)
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; Pred. No. 1.3e-106;
10; Mismatches 27;
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91.8%;
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Best Local Similarity 91.89
Matches 550; Conservative
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295 KGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASG
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GenCore version 4.5
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OM protein - protein search, using sw model

July 3, 2002, 08:36:25; Search time 104.77 Seconds (without alignments) 627.619 Million cell updates/sec

US-09-771-382-10 2988 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 592 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

747574 Total number of hits satisfying chosen parameters: 747574 seqs, 111073796 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A\_Geneseq\_032802:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					))	
		æ				
Result		Query				
No.	Score	Match	Match Length DB	DB	ΩI	Description
-	2988	100.0	592	22	AAU06180	N. meningitidis 22
7	2942	98.5	592	20	AAY27203	Amino acid sequenc
3	2779	93.0	592	20	AAY23744	A surface protein
4	2779	93.0	592	22	AAU06172	N. meningitidis H4
5	2626.5		589	20	AAY23745	A surface protein
9	2626.5		589	22	AAU06173	N. meningitidis P2
7	2587.5		599	20	AAY23743	A surface protein
æ	2587.5		599	22	AAU06176	N. meningitidis H3
6	2552		594	20	AAY23739	A surface protein
10	2552	85.4	594	22	AAU06179	N. meningitidis BZ
11	2533		594	20	AAY23740	A surface protein

Region

BASB029 amino acid N. meningitidis EG A surface protein N. meningitidis H1 A surface protein N. meningitidis B2	BASB029 amino acid Amino acid sequenc A surface protein N. meningitidis PM A surface protein N. meningitidis EG	surface protei . meningitidis . meningitidis . meningitidis . meningitidis . meningitidis	adhe adhe infl adhe infl infl	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
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12 13 15 16		42222 4222 4200 4300 4300		5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

## ALIGNMENTS

N. meningitidis 22491 surface antigen NhhA polypeptide sequence. Surface antigen NhhA; meningococcal disease; meningitis vaccine. Location/Qualifiers
1.50
//label= C1
//note= "Conserved region 1"
51.102
//label= V1
//note= "Variable region 1" 125.188
/label= C3
/note= "Conserved region 3"
189.208
/note= "Variable region 3"
209..227 /label= C2
/note= "Conserved region 2" 5 115..124 /label- V2 /note- "Variable region Neisseria meningitidis strain 22491 AAU06180 standard; Protein; 592 AA. (first entry) .114 24-0CT-2001 AAU06180; Region Region Region Region Region Region AAU06180 

480 540

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The invention provides proteins (AAY27201-245) from Neisseria meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167) or antibody specific to the protein are useful as pharmaceuticals, e.g. a vaccine composition or a diagnostic composition. The composition is also useful for treating or preventing an infection due to Neisserial bacteria, especially Neisseria meningitidis.
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                                                             tdegeglvtakevidavnkagwrmktttangqtgqadkfetvtsgtnvtfasgkgttatv
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Pred. No. 2.8e-163;
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98GB-0019015.
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N-PSDB; AAX99125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -
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/label= C4
/note= "Conserved region
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/label= V4
/note= "Variable r
237..592
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/label= C5
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Matches 592; Conservative
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meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to use form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                 Claim 1; Page 118-120; 132pp; English.
meningitidis infections
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                                                                                                   GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDF
                                                                                                                                                                      TDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATV
                                                                                                                                                                                                       SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV
                                                                                                                                                                                                                                        NINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPV
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                                                                                                                                                                                                                                                                                                                   treating
                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; surface glycoprotein; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis surface proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                        meningitidis
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                                                                                                                                                                                                                                                                                                                                                                                                                       surface protein of Neisseria
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                            Gaps
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                                                                      DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGENG
                                                                                                                                                                                                                                                                                         SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA
                                                                                                                                                                                                                                                                                                                                          TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                                                                                                                                                                                                                                                                                 TVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVRITINVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
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                                                                                                         ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT
                                                                                                                                                                 NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNI I SDTKGLNFAKETAGTNGDTTVHLN
                                                                                                                                                                                                                     GIGSTLTDTLAGSSASHVDAGNQST - - HYTRAASIKDVLNAGWNIKGVKTGSTTGQSENV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Surface antigen NhhA; meningococcal disease; meningitis vaccine.
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 592;
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                            Indels
Score 2779; DB 20;
Pred. No. 8.4e-154;
); Mismatches 23;
                            9; Mismatches
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93.0%;
llarity 93.9%;
Conservative
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            Best_Local Similarity
Matches 558; Conserv
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592 AA;

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Neisseria meningitidis strain H41.
                                                                                                      /label= V3
/note= "Variable
                                                                                                                                                                                                                                Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                              25-JAN-2000; 2000US-0177917.
                                                                                                                                                                     25-JAN-2001; 2001WO-AU00069
                                       label- V1
                                                                                                                              /label≈ V4
                                                                          124
                                                                                                              .229
                                                                                      188
                                                                                                  189..210
                                   ...102
                                                                                                                                                                                      (UYQU ) UNIV QUEENSLAND
                                                                                                                                                                                             Peak IRA, Jennings MP;
                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                                                                                                    WPI; 2001-488774/53.
N-PSDB; AAS09162.
                                                              103
                                                                                                                                                     WO200155182-A1
                                                                                                                                                             02-AUG-2001
              Peptide
                                               Protein
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                       Region
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418
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                                                                                                                                                                                                                            SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 358
                                                                                                                                          ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT 120
                                                                         Gaps
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                                                                                                                                                                                                                                                                          GIGSTLTDTLAGSSASHVDAGNQST - - HYTRAASIKDVLNAGWNIKGVKTGSTTGQSENV
                                                                                                                                                                                                                                                                                           DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENG
                                                                                                                                                                                                                                                                                                                                                          359 TVSKDDQCNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 KSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 592
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             Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Surface protein; surface glycoprotein; infection; vaccine;
                                              Indels
          Score 2779; DB 22;
Pred. No. 8.4e-154;
9; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A surface protein of Neisseria meningitidis.
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             93.0%;
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                              Best Local Similarity 93,9
Matches 558; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoreactive peptide
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                 Query Match
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                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence representing the wild type surface antigen Nhha from N. meningitidis strain H41 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                              /note= "Predicted mature protein, specifically
claimed in claim 12"
                                                             /label= Cl
/note= "Conserved region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                  //11.....
//label= C4
/note= "Conserved region 4"
                                                                                                                                                                                                                             /label= C2
/note= "Conserved region 2"
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/note= "Conserved region 3"
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237..592
                                                                                                                              'note= "Variable region 1"
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/note= "Conserved region
                                                                                                                                                                                                                                                                           /label= V2
/note= "Variable region
                 1..51
/label- Signal_peptide
                                                                                                                                             52..592
/label= Mature_NhhA
Location/Qualifiers
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/label= Cl /label= Cl /^abel= Conserved region l"

Location/Qualifiers

Tabel = C3 'note= "Conserved region 3"

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"Variable region

/label= V3

/note=

205

/label= C4 /note= "Conserved region"

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"Conserved region

/label= C2

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'note= "Variable region

.185

/label=

/label= V2

121

/note=

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/label= V1 /note= "Variable region

5

'note= "Conserved region

/label= C5 /note= "V 234..589

region 4"

/label= V4 /note= "Variable

225..233

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Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                           N. meningitidis P20 surface antigen NhhA polypeptide sequence
                                                                                                           Neisseria meningitidis strain P20
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                                   24-OCT-2001
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             AAU06173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGE 296
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                   1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60
                                                                                                                                          The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kps. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            537 PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 592
                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                        DB 20; Length 589;
                                                                                 Neisseria meningitidis surface proteins useful for treating N.
                                                                                                                                                                                                                                                                                                                               41; Indels
                                                                                                                                                                                                                                                                                                     ; Score 2626.5; DB 2;
; Pred. No. 6.1e-145;
13; Mismatches 41;
                                                                                                                                                                                                                                            used to identify immunoreactive peptides.
                                                                                                                     Claim 1; Page 122-124; 132pp; English.
                         Peak IRA;
                                                                                                                                                                                                                                                                                                     87.9%;
89.1%;
                                                                                                                                                                                                                                                                                                                             Matches 531; Conservative
(UYQU ) UNIV QUEENSLAND
                                                                                             meningitidis infections
                       Moxon
                                             WPI; 1999-418754/35.
N-PSDB; AAX85797.
                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                   589 AA;
                       Jennings MP,
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                        Query Match
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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhA (AA066182-AAU06186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain P20 is 1 of 10 NhhA polypeptide sequences ö New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating preventing broad spectrum of Neisseria meningitidis -Claim 9; Fig 1; 91pp; English.

AAU06173 standard; Protein; 589 AA

AAU06173

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surface proteins useful for treating

Peak

Moxon ER,

LTD.

INNOVATION QUEENSLAND.

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The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                 1; Page 114-115; 132pp; English
                                                                                              meningitidis infections
                                                                                     Neisseria meningitidis
                                                        WPI; 1999-418754/35
                                                                                                                                                                                                                                       599 AA;
                                                                  N-PSDB; AAX85795
       ISIS
                                    Jennings MP,
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                   Query Match
       (ISIS-)
(UYQU)
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(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
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                                                                                                                                     ESVQRS-VVGSIQASMEGSGELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNT 116
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                                                                                                                                                                                                                               NGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGT
                                                                                                                                                                                                                                                                                                            NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGE
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                                                                                                                                                         esvarsalvlqfmidkegngeiestgdigwsiyyddhntlhg-atvtlkagdnlkikg--
                                                                                                          PGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface glycoprotein; infection; vaccine;
                                                                            Indels
                                                         22;
                                                      ; Score 2626.5; DB 2;
; Pred. No. 6.1e-145;
13; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of Neisseria meningitidis
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                                                        87.9%;
89.1%;
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                                                         Query Match
Best Local Similarity 89.19
Matches 531; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunoreactive peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis
          the present invention.
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                                                                                                                                61 ESVQRS-VVGSIQASMEGSGELET---ISLSMINDSKEFVDPYIVVTLKAGDNLKIKQ--
                                                                                                                                                                                                                                                                                                       351 ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALN
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                                                                                                                                                                                                                              GDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIKGVKTGS
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                                                         1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                       DB 20; Length 599;
                            44; Indels
86.6%; Score 2587.5; DB 2
88.0%; Pred. No. 1.2e-142;
                            15; Mismatches
                Best Local Similarity 88.03
Matches 530; Conservative
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9 9 114

172

230 239 290 297 350 357 410 417 470 477 530 537 590 597

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medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain 138 is 1 of 10 Nhh polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
                                                                                                                                                                                                                                                                                                                                                        61 epvvrsalvlqfmidkegngenestgnigwsiyydnhntlhg-atvtlkagdnlkikqnt 119
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                                                                                                                                                                                                                                                                             13;
   and in designing and/or screening
                                                                                                                                                                                              DB 22; Length 599;
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                                                                                                                                                                                            86.6%; Score 2587.5; DB 22; Lengt
88.0%; Pred. No. 1.2e-142;
.ive 15; Mismatches 44; Indels
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 meningitidis,
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                                                                                                                                                                                            Query Match 86.6
Best Local Similarity 88.0
Matches 530; Conservative
                                                                                                                 the present invention
                                                                                                                                                 599 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -
                                                                                                                                                                                                             Surface antigen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                            N. meningitidis H38 surface antigen NhhA polypeptide sequence
                                                                                                                                                                                                                                                                                  /label= Cl
/label= Cl
...tam "Conserved region 1"
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note= "Conserved region 2"
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                                                                              AAU06176 standard; Protein; 599 AA.
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note= "Variable
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/label= V2
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/label= C5
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/label= v1
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/label= V4
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                                             469 LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
            Surface antigen NhhA; meningococcal disease; meningitis vaccine.
                                                                                                                                                                                                                                                         meningitidis B2198 surface antigen NhhA polypeptide sequence
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/label= V1
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|591 gygw 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGN 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to be used to use to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 GSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 594;
                                                                                                                                                                                                                                 Neisseria meningitidis surface proteins useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4%; Score 2552; DB 20;
86.8%; Pred. No. 1.3e-140;
ilve 16; Mismatches 42;
                                                                                                                                                                                                                                                                   Claim 1; Page 95-97; 132pp; English.
                                                                                                                                                                     Peak IRA;
                                                                                  98WO-AU01031.
                                                                                                                                   LTD.
                                                                                                         97GB-0026398
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                                                                                                                                 INNOVATION
                                                                                                                                                                     Jennings MP, Moxon ER,
                                                                                                                                             QUEENSLAND
                                                                                                                                                                                                                                            meningitidis infections
           Neisseria meningitidis.
                                                                                                                                                                                           WPI; 1999-418754/35.
N-PSDB; AAX85791.
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Best Local Similarity
Matches 524; Conserv
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                                                meningitidis mutant polypeptides of the surface antigen NhA
(AAU06182-AAU06186). The modified or mutant NhA polypeptides are
characterised by deletions of non-conserved amino acids, particularly
the deletion of variable regions. The deletion mutants are useful in
diagnostics, therapeutic and prophylactic vaccines against a broader
spectrum of N. meningitidis, and in designing and/or screening of
medicaments. The mutant proteins when used as a vaccine can effectively
immunise against a broader spectrum of N. meningitidis strains than
would be expected from a corresponding wild-type surface antigen.
The present sequence representing the wild type surface antigen NhhA
from N. meningitidis strain B1298 is 1 of 10 NhhA polypeptide sequences
(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
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                                                                                                                                                                                                                                                                                                                                  KIKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAG 170
                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                       1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGN
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                                                                                                                                                                                                                                   Length 594;
                                                                                                                                                                                                                                                       Indels
                                        present invention relates to the isolation of novel
preventing broad spectrum of Neisseria meningitidis
                                                                                                                                                                                                                                 85.4%; Score 2552; DB 22;
86.8%; Pred. No. 1.3e-140;
                                                                                                                                                                                                                                                      16; Mismatches
                   Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                             Best Local Similarity 86.89
Matches 524; Conservative
                                                                                                                                                                              the present invention.
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GKGKCENGSSTDEGEGLYTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF 350
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                                                                                                                                                                                     Surface protein; surface glycoprotein; infection; vaccine;
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86.4%; Pred. No. 1.7e-139;
ive 20; Mismatches 44;
                                                                                                                                      surface protein of Neisseria meningitidis
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AAY23740 standard; Protein;
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                                                                                                                                                                                                              immunoreactive peptide
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Matches 520; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the Nisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the Haemophilus influenzae surface fibril (HSF) protein. The invention relates to BASB029 polymucleotide sequences (AAZ39864-239865) and polypeptide sequences (AAZ57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of
                                                                                                                                                                                                                                                                                                                                           BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
infection; treatment; prevent; antibacterial drug.
                              470
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                                                                                                                           532
                                                                                                                                               590
                                                                                                                                                                   592
 gkdkgendsstdkgeglvtakevidavnkagwrmktttangqtggadkfetvtsgtnvtf 352
                                                             PSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                  LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY
                                                                                                                                                                                                                                                                                                                           amino acid sequence from N. meningitidis strain ATCC13090
                     ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                      VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide from neisseria meningitidis useful for di
treatment or prevention of bacterial infections in mammal
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Encoded by AATC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                              AAY57044 standard; Protein; 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 2; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-EP03255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0010276
                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-053103/04.
N-PSDB; AAZ39864.
                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9958683-A2
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qw 594
                                                                                                                                                                                                                                                                                                       21-FEB-2000
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                                                                                                                                                                                          QW 592
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                                                                                                                                                                                                                                                                                    AAY57044;
                                                                                                                                                                                                                                                                                                                            BASB029
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the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASBO29 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Rused recombinant protein is useful for the stimulation of the immune system of an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410
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                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                       PSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                                                                                                                                                                                                                                                                                                                            ESVQR-SVVGSIQASMEGSGELETISLSMTNDS-----KEFVDPYIVVTLKAGDNLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KONTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST -- HYTRAASIKDVLNAGWNIKGVKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meningitidis EG327 surface antigen NhhA polypeptide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Surface antigen NhhA; meningococcal disease; meningitis vaccine
                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                            Length 594;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                          Score 2533; DB 21;
Pred. No. 1.7e-139;
); Mismatches 44;
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                                                                                                                                                                                                                                          84.8%; Scor
86.4%; Pred
tive 20; I
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                                                                                                                                                                                                                                                                                      Matches 520; Conservative
                                                                                                                                                       receiving the protein.
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                           594 AA;
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. Mon Jul

9:

Gaps 9

18;

112

172

230 234 290 292

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(UYQU ) UNIV QUEENSLAND
                                                                                          Peak IRA, Jennings MP
                                                                                               WPI; 2001-488774/53.
N-PSDB; AAS09164.
                                                                     WO200155182-A1
                                                                         02-AUG-2001
                                                                                                                                                   Sequence
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epvqrtavvlsfrsdkegtgeke----vtedsnwgvyfdkkgvltagtitlkagdnlki 114
                                                                                                                                                               PSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALN 470
                           KONTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTN
                                                                                                                                                                                                         GDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST - - HYTRAASIKDVLNAGWNIKGVKTGS
                                                                                                                                                                                                                                                                     TTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT
                                                                                                                                                                                                                                                                                  ta--sdnvdfvrtydtveflsadtktttvnveskdngkrtevkigaktsvikekdgklvt
                                                                                                                                                                                                                                                                                                                              GKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
                                                                                                                                                                                                                                                                                                                                              ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQA1ATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESVQR-SVVGSIQASMEGSGELETISLSMTNDS-----KEFVDPYIVVTLKAGDNLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          surface glycoprotein; infection; vaccine;
44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A surface protein of Neisseria meningitidis.
20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ISIS-) ISIS INNOVATION LTD. (UYQU ) UNIV QUEENSLAND.
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Matches 520; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surface protein; surfactimmunoreactive peptide
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gw 594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen NhhA from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NhhA surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2533; DB 22; Length 594;
Pred. No. 1.7e-139;
                                                                                      /noce.
51..104
/label- Vl
^nte= "Variable region 1"
                                                                                                                                                                                                                                                                    /note-
|191..212
|/label= V3
|`^te= "Variable region 3"
                                                                                     -
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= C5
/note= "Conserved region 5"
                                                                                                                                                                           region 2"
                                                 //label= Cl
//abel= Cl
/~ate= "Conserved region 1'
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                                                                                                                                                                                                                                  27..190
label C3
note= "Conserved region"
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/note= "Conserved region
                                                                                                                                                                                                      Tabel = V2
                                                                                                                                                                                                                                                                                                                                                                                        'label= V4
'note= "Variable region
             Neisseria meningitidis strain EG327.
                                         Location/Qualifiers
                                                                                                                                                                          "Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Fig 1; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.8%;
86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JAN-2001; 2001WO-AU00069
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                                                                                                                                                             C_2
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                                                                                                                                                               label-
                                                                                                                                                                           'note=
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Best Local Similarity
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412

530

532

472

590

410

352

598 AA.

(first entry)

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AAU06177 standard; Protein;
                                          24-OCT-2001
                         AAU06177;
AAU06177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ESVQR-SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYI------VVTLKAGDNL 110
                                                                                                                                                                                                                                                                                      KIKQNTNENTNA----SSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKV 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            524
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                                                                                                                                                                                                                                                                                                                                               ETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISGNVSPSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVD 464
                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                         59
                                                                                                                                                                                                                                        1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60
                                                                                                                                                                                                                                                 The present sequence represents a surface protein of Neiserria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.
                                                                                                                                                                                                                                                                                                                                                                                           DEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGA
                                                                                                                                                                                                                                                                                                                                                                                 GVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEK
                                                                                                                                                                                                                                                                                                                                                                                                                    DGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTS
                                                                                                                                                                                                                                                                                                                      26;
                                           ż
                                                                                                                                                                                                     Length 598;
                                          surface proteins useful for treating
                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                        45;
                                                                                                                                                                                                     84.5%; Score 2524; DB 20;
85.5%; Pred. No. 5.7e-139;
tive 17; Mismatches 45;
                                                                     English
Peak IRA;
                                                                    Claim 1; Page 108-110; 132pp;
                                                                                                                                                                                                                       Conservative
                                          Neisseria meningitidis meningitidis infections
Moxon ER,
               WPI; 1999-418754/35
N-PSDB; AAX85794.
                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 520; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SASVGYQW 592
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Jennings MP,
                                                                                                                                                                             Sequence
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RESULT

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The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen NhA (AANO6186-AANO6186). The modified or mutant NhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of N. meningitidis strains than would be expected from a corresponding wild-type surface antigen.
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                                            disease; meningitis vaccine
N. meningitidis H15 surface antigen NhhA polypeptide sequence.
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/note= "Conserved region 4"
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                                              Surface antigen NhhA; meningococcal
                                                                                                                                          Location/Qualifiers
                                                                                           Neisseria meningitidis strain H15.
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N-PSDB; AAS09167.
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The present sequence representing the wild type surface antigen NhhA from N. meninglitidis strain H15 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different N. meningitidis strains given in the present invention.
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                                                                                                                                                                      ETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIK 224
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                                                                               Length 598;
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                                                                            84.5%; Score 2524; DB 22;
85.5%; Pred. No. 5.7e-139;
iive 17; Mismatches 45;
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Best Local Similarity
Matches 520; Conserv
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OM protein - protein search, using sw model

July 3, 2002, 08:37:11; Search time 39.66 Seconds (without alignments) 364.598 Million cell updates/sec ö

US-09-771-382-10 2988 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 592 Perfect score:

Scoring table: Sequence:

231628 seqs, 24425594 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Match Length	å Query Match Length			DB	SUMMAKLES ID	Description
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93.0 592 4	592 4	4	4 US-	-Sn	US-09-669-974-17	
87.9 589 4	589 4	4	4 US	ns	US-09-377-155-19	19,
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85.4 594 4	594 4	4	4 05	Ď	US-09-377-155-7	7, 4
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84.4 598 4	598 4	4	4 U.S	Ď	US-09-669-974-5	Ŋ,
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81.8 591 4	591 4	4	<b>4</b> U	D	US-09-377-155-11	11,
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1132.5 37.9 2353 4 U	4	4	4 0	כ	US-09-377-155-33	Sequence 33, Appl

Sequence 4, Appli	Sequence 33, Appl	Sequence 47, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 36, Appl	Sequence 6, Appli	9	9	Sequence 4, Appli	Sequence 4, Appli	Sequence 15, Appl	Sequence 26, Appl	Sequence 32, Appl	Sequence 24, Appl	30, 7	Sequence 28, Appl
US-08-913-942-4	US-09-669-974-33	US-09-268-347-47	US-08-409-995-5	US-08-685-467-5	US-08-913-942-5	US-09-268-347-36	US-08-409-995-6	US-08-685-467-6	US-08-913-942-6	US-08-409-995-4	US-08-685-467-4	US-08-913-942-15	US-09-268-347-26	US-09-268-347-32	US-09-268-347-24	US-09-268-347-30	US-09-268-347-28
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37.9	37.9	37.9	37.5	37.5	37.5	36.9	35.5	35.5	35.5	35.5	35.5	33.5	33.5	32.6	24.4	24.1	22.3
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## ALIGNMENTS

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ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT 120
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93.0%; Score 2779; DB 4;
Best Local Similarity 93.9%; Pred. No. 2.4e-207;
Matches 558; Conservative 9; Mismatches 23;
                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 17
                                                              APPLICANT: PEAK, Ian Richard Anselm APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
            Sequence 17, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Neisseria meningitidis US-09-377-155-17
US-09-377-155-17
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299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTKVTFASGNGTTA 358
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                                                                                          TVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
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                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR PAPLICATION NUMBER: PCT/AU98/01031
PRIOR PILING DATE: 1998-12-14
PRIOR PILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/09377155 Patent No. 6197312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Neisseria meningitidis
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APPLICANT: PEAK, Ian Richard
APPLICANT: JENNINGS, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTA 358
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DFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENG
                                                                                                                          PVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPG
                                                                                                                                                                                        TVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDE
                                                                                                         TVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANK
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Pred. No. 2.4e-207
9; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENITON: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 592
; TYPE: PRT
; ORCANISM: Neisseria meningitidis
US-09-669-974-17
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Best Local Similarity 93.9%;
Matches 558; Conservative
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   354 TATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKM 413
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                                  DETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDA
                                                                                                                                                             1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
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Pred, No. 1.7e-192;
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                                                                                                                                                                                                                                                                                                                                                                              ON: NOVEL SURFACE ANTIGEN 065064/0128
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
                                                                                                                                                                                                                                                                                                                         APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE AN
FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                             Sequence 15, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION: APPLICANT: PEAK, Ian Richard Anseln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis
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88.0%;
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Best Local Similarity 88.0%
Matches 530; Conservative
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                                                                                                                                                                                                                                                             US-09-377-155-15
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US-09-377-155-15
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                                                                 VHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSE
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                                                 DETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 87.9%; Score 2626.5; DB 4 Best Local Similarity 89.1%; Pred. No. 1.6e-195; Matches 531; Conservative 13; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/377,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: BCT/AU98/01031
PRIOR FILING DATE: 1997-12-12
NUMBER: OF SEQ ID NOS: 33
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                             US-09-669-974-19; Sequence 19, Application US/09669974; Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Neisseria meningitidis
US-09-669-974-19
                 354
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VTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNV 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ESVQR-SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYI------VVTLKAGDNL 110
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                                              VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                                            171 INGDITVHLNGIGSTLIDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIKGVKT
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                               PSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALN
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86.8%; Pred. No. 9.5e-190;
ive 16; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXOW, E. Richard
TITLE OF INVENTION: NOVEL SUFFACE ANTIGEN
FILE REFERENCE: 065064/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCTAU98/01031
PRIOR FILING DATE: 1998-12-14
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UMBER: GB 9726398.
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; ORGANISM: Neisseria meningitidis
US-09-377-155-7
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PRIOR FILING DATE: 1997-12-12
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US-09-377-155-7
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SEQ ID NO 7
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                                                VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
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s; Pred. No. 1.7e-192;
15; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                    APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: DENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR PELICATION NUMBER: US/09/317,155
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-11/4098/01031
PRIOR FILING DATE: 1999-11/4098/01031
PRIOR FILING DATE: 1999-12-12
PRIOR APPLICATION NUMBER: GB 9726398.2
NUMBER OF SEO ID NOS: 33
                                                                                                                                                                                                                                                                                       Sequence 15, Application US/09669974 Patent No. 6333173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Neisseria meningitidis US-09-669-974-15
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88.0%;
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Best Local Similarity 88.0'
Matches 530; Conservative
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LENGTH: 599
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                                                ESVQR-SVVGSIQASMEGSGELETISLSMTNDS-----KEFVDPYIVVTLKAGDNLKI
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                                349 TFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGN
                                                                                           VSPSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGA
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86.4%; Pred. No. 2.8e-188;
iive 20; Mismatches 44;
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APPLICANT: JENINGS, Michael Paul
APPLICANT: JENINGS, Michael Paul
APPLICANT: JENINGS, MICHAEL
TILE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09377155 Patent No. 6197312
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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Best Local Similarity 86.4%
Matches 520; Conservative
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LNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT
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; Pred. No. 9.5e-190;
16; Mismatches 42;
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CURRENT FILING DATE: 2000-09-26

PRIOR APPLICATION NUMBER: US/99/669,974

CURRENT FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-12-14

PRIOR FILING DATE: 1998-12-14

SOFTWARE: PALENTING DATE: 1997-12-12
                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09669974 Patent No. 6333173
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86.8%;
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591 GYQW 594
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                                                                                                             1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
TA--SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVT
                                                293 GKDKGENDSSTDKGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
                                                                                              ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVS
                                                                                                                                                             PSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALN
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                                 GKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF
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85.5%; Pred. No. 1.4e-187;
ive 17; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: PEAK, Ian Richard Anselm APPLICANT: PEAK, Michael Paul APPLICANT: JENNINGS, Michael Paul APPLICANT: MOXON, E. Richard Paul TITLE OF INVENTION: NOVEL SURPACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR APPLICATION NUMBER: GB 9726398.2
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 13, Application US/09377155 Patent No. 6197312 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ve
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                                                                                                                                   VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: PEAK, Ian Richard Anselm, APPLICANT: DENNINGS, Michael Paul, APPLICANT: DENNINGS, Michael Paul, APPLICANT: DENNINGS, Michael Paul, APPLICANTON MOXON. E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT APPLICATION NUMBER: US/09/679,77,155
PRIOR FILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
PRIOR PLILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALCHIN Ver. 2.0
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US-09-669-974-9
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US-09-669-974-9
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Patent No. 6197312
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: GB 9726398.2
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
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291 DGKLVTGKGKDENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTS
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                                                                                                                       GTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKV
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85.5%; Pred. No. 1.4e-187;
ive 17; Mismatches 45;
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Patent No. 6333173
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Matches 520; Conservative
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US-09-669-974-13
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113 KIKQNTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAK 172
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                                 ETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST - - HYTRAASIKDVLNAGWNIK
                                                                                              GVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEK
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CURRENT APPLICATION NUMBER: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1998-12-12
PRIOR FILING DATE: 1998-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET. 2.0
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84.2%; Pred. No. 5.7e
iive 30; Mismatches
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Matches 506; Conservative
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US-09-377-155-21
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LENGTH: 591
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                                                                                                                                                                                                                                                                                                                                                                          DGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTS
                                                                                                                                   345 GTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKV
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; Pred. No. 2.4e-187;
16; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: PERA JAN RICHARD ANSELM APPLICANT: PERA JAN RICHARD PAUL APPLICANT: DENNINGS, Michael Paul APPLICANT: DENNINGS, Michael Paul APPLICANT MOXON. E. Richard TITLE OF INVENTION: NOVEL SURFACE ANTIGEN FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-08-19
PRIOR PLICATION NUMBER: PCT/AU98/01031
PRIOR PLICATION NUMBER: GB 9726398.2
PRIOR PELING DATE: 1997-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PALCHIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09669974 Patent No. 6333173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Neisseria meningitidis US-09-669-974-5
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Best Local Similarity 85.55
Matches 520; Conservative
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591 SASVGYQW 598
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SOFTWARE: POLY
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LENGTH: 598
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120 Q-----NGTNFTYSLKKDLTDLTSVGTEKLSFSANGNKVNITSDTKGLNFAKETAGTNG 173
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                                                     234 A--SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTEVKIGAKTSVIKEKDGKLVTG 291
                                                                                                   SGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSP 411
                                                                                                                            174 DTTVHLNGIGSTLTDTLAGSSASHVDAGNQST -- HYTRAASIKDVLNAGWNIKGVKTGST
                                              232 TGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTG
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Search completed: July 3, 2002, 08:37:13 Job time: 339 sec ٠.

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OM protein - protein search, using sw model

Run on:

July 3, 2002, 08:38:32; Search time 58.79 Seconds (without alignments) 967.595 Million cell updates/sec

US-09-771-382-10 2988 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 592 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters: 283138 seqs, 96089334 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	probable surface f	adhesin NMB0992 [i	adhesin homolog HI	surface protein XF	surface protein XF	probable autotrans	probable adhesin Z	probable adhesin E	probable surface p	surface-exposed on	ydeK protein - Esc	hypothetical prote		probable exported	AidA-I adhesin-lik		probable adhesin h	probable adhesin P	hypothetical prote		hypothetical prote	adhesin AIDA-I pre		hypothetical prote		c	high-molecular-wei	hypothetical prote	surface-array prot
ID	A81888	G81133	I64138 .	D82671	A82615	AC0976	A86036	н91188	AH0110	C82672	A64905	E90893	D85724	AH0038	D90803	н85611	AF0394	Н83135	A83080	T33369	T31105	S28634	B85547	AC2224	AH2515	140711	B43855	F90696	A56143
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Length	592	591	298	2059	1190	1107	1588	1588	658	1004	1325	1343	1343	1238	949	1005	1910	1018	1417	1275	4919	1286	5188	1428	4936	936	1477	5291	1109
% Query Match	100.0	82.5	18.8	13.7	13.2	12.6	12.5	12.5	11.4	8.4	8.3	7.7	7.6	7.4	7.3	7.3	7.3	7.3	7.1	7.0	7.0	7.0	7.0	7.0	7.0	7.0	6.9	6.9	6.9
Score	2988	2464.5	561	410.5	394.5		373.5		341.5	10		231.5	227.5	220.5	219.5	219.5	219.5	219	212	210.5	210.5	210	209.5	209	209	208.5	207.5	207.5	202
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:204	203.5	198.5	197	197 196.5	196 195.5	195.5	193	193
30 31	33.2	33 G	37	38 30 8	40.41	42	4 <b>4</b> 0 <b>4</b>	45

## ALIGNMENTS

(strain Z , S.R.; Mo ; Rajandre idis 22491	; PID:9737	0;							
idis 2001 Xlee M.A.	61.1	Gaps	09	120	180	240	300	360	420
RESULT 1 A81888 probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: A81888 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre Nature 404, 502-506, 2000 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491 A:Reference number a81775; MITD: 2022556	A,Accession: AB1888 A,Status: preliminary A,Mcdeus: type: DNA A,Mcdeus: 1-592 cPAR> A,Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737 A,Experimental source: serogroup A, strain 22491 C;Genetics: A,Gene: NMA1200	Query Match 100.0%; Score 2988; DB 2; Length 592; Best Local Similarity 100.0%; Pred. No. 6.7e-146; Matches 592; Conservative 0; Mismatches 0; Indels 0; Ga	QY 1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL	Qy 61 ESYQRSVYGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT	OY 121 NASSETYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGINFAKETAGTNGDTTVHLN 	QY 181 GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGGSENVDF	QY 241 VRTYDTVEFLSADFKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGRGENGSS 	QY 301 TDEGEGLYTAKEVIDAVNKAGWRMKTTTANGGTGQADKEETVTSGTNVTFASGKGTTATV	OY 361 SKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETV 420
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C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: D82671
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucle
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Note: for a complete list of authors see reference number A59328 below
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                                                                                                                                           GSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGL
                             VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQ
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43.1%; Pred. No. 6e-22;
Live 34; Mismatches 86;
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B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                 adhesin NMB0992 (imported) - Neisseria meningitidis (strain MC58 serogroup B)
C.Species: Neisseria meningitidis
C.Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
R.Pettelin, H.; Saunders, N.J.; Heldelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
L.; A., Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.
A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Rapterence number: A81000; MUID:20175755
A.; Reference number: A81000; MUID:20175755
A.; Residues: preliminary
A.; Mosidues: 1-591 
A. Mosidues: 1-591 
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                                     RITHVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKS
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; Pred. No. 4.4e-119;
30; Mismatches 46;
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ilarity 84.2%;
Conservative 3
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A) Gene: NMB0992
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Best Local Similarity
Matches 506; Conserv
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A. Experimental Source: Strain 945c
Risimpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Rainaco, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Rarones, A.J.G.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. submitted to GenBank, June 2000
A.A. Frora. Franca, S.C.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigt chado, M.A.; Madeira, M.M.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matsukuma, A.Y.; Monck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Palmieri, D.A. A.Authors: da Silva, A.C.R.; de Silva, F.R.; de Silva, A.M.; Silva Jr., W.A.; de Silva, A.M.; Silva Jr., W.A.; de Silva, A.M.; Silva Jr., W.A.; de Silvaira, M.R.; de Salvaira, M.R.; Salvaira, M.
                                                                                                  Residues: 1-2059 <SIM>
Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
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EFTDAVNFSQLKSISTAVDQGW---TLTASGANGSK--VASGGTVDLKNTDGNLTISKSG 1456
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A; Accession. ....
A; Status: preliminary
A; Molecule type: DNA
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C;Genetics:
A;Gene: XF1529
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surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
S;Sincy Xylella fastidiosa
S;Status: Xylella
S;S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               646 VDSLTTGNTAMTTDGVTVGSNVTLGSTGLVITDGPSVTSSGISAGNQKITNVAAGTADTD
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Gene: XF1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        801
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---PTLSVDDE

----NVADAKEAT--DAVNLRQLDRVAQDANRYVDNKIESLSEGQTF------

ETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADA----

KDDQGNITVMYDVNVGDALNVNQL----QNSGWNLDSKAVAGSSGKVISGNVSPSKGKMD

Qγ

QY       379 ALNVN	Db 93.2 RITNIVAAGVNNTDAVNVAQLKASEAGSVRYETNADGSVNYSVLNLGDGSGGTTRIGNVSA 991  Qy 50.2GVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYL 536	RESULT 7 A86036 probable adhesin 25029 [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C;Accession: A86036 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May 111er, L.; Grotheeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551	A.Kacess.der. 200030 A.Status: preliminary A.Molecule type: DNA A.Residues: 1-1588 <sto> A.Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP: A.Experimental source: strain 0157:H7, substrain EDL933 C:Genetics: A;Gene: 25029</sto>	Query Match 12.5%; Score 373.5; DB 2; Length 1588; Best Local Similarity 23.1%; Pred. No. 2.2e-11; Matches 176; Conservative 95; Mismatches 261; Indels 231; Gaps 30; Qy 7 IIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60 C) 11	61 ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLK 11  81	161 GLNFAKETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDV 161 GLNFAKETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDV 1034 IINQLAGNTDATYIQENGAGINYVRTNDDGLAFNDASAQGVGATAIGYNSVAKGDSS 217 LNAG-WNIKGVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIG 1	DD 1091 VALGGGSYSDVDTGLALGSSSVSSRVTAKGSKDTSIIENGVVIG 1134  QY 276 AKTSVIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRM 324   :
Db 1004VKVNSLNNSATPIAAGVDATAIGVGATASGADSIAMGNKASASADNA 1050  Qy 467 GALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNV 514	RESULT 6 AC0976 probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar T C:Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C:Date: 09-Nov-2001 C:Dat	Nature 413, 848-852, 2001 A) Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Reference number: AB0502; PMID:11677608 A; Accession: AC0976 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-1107 < PAR> A; Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176 C; Genetics: A; Gene: sapB	Ouery Match 12.6%; Score 375.5; DB 2; Length 1107;  Best Local Similarity 22.0%; Pred. No. 1.1e-11;  Matches 184; Conservative 103; Mismatches 232; Indels 317; Gaps 36;  Qy 9 WNSALNAWVAVSELTRNHTKRASATVKTAVLATLEFATVQANA 51	Qy 52 TDEDEEEELESVQRSVVGSIQASMEGS-GELE 82	Qy       140 ETEKLSFGANGKKVNIISDFKGLNFAKE-TAGTNGDTTVHLNGIGSTLTDTLAGSSASHV 198         1:	QY         246 TVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGEN 297	Qy 336ADKFETVTSGTNVTFASGKGTTATUSKDDQGNITVMYDVNVGD 378

Db 1135 YDTT;-DGELLGALSIGDDGKYRQIINVADGSEAHDAVTVRQLQNAIGAVATTPTKY 1  Db 1190 FHANSTEEDSLAVGTDSLAMGAKTIVNGDKGIGIGYGAYVDANALNGIAIGSNAQVIHVN 1  Qy 349 TFASGKGTTAT	1189 348 1249 1366 1366 1440 1440 1485	Db 1091 VAIGGGSYSDVDTGIALGSSSVSSRVIAKGSRDTSITENGVVIG 1134  Qy 276 AKTSVIKEKDGKLUTGKGKGENGSSTDEGEGLUTAKEVIDAVNKAGWRM 324
RESULT 8 H91188 robable adhesin ECs4480 [similarity] - Escherichia coli (strain 0157:H7	H7, substrain RIME	QY 550 RGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVGYQW 592 
C;Specias Escherichia coll C;Specias Escherichia coll C;Specias Escherichia coll C;Specias Escherichia coll C;Accession: H91188 R;Haysahi, T;Makino, K;Ohnishi, M;Kurokawa, K;Ishii, K;Yokoyama, K;Haysahi, T;Makino, X;Yohnishi, M;Kurokawa, K;Hattori, M;Shinagawa, H. DNA, Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coll O157:H7 & A;Title: Complete genome sequence of enterohemorrhagic Escherichia coll O157:H7 & A;Title: Complete genome sequence of enterohemorrhagic Escherichia coll O157:H7 & A;Title: Complete genome sequence of enterohemorrhagic Escherichia coll O157:H7 & A;Title: Complete genome sequence of enterohemorrhagic Escherichia coll O157:H7 & A;Title: DNA A;Title	7-2001 Jawa, K.; Han, C.G. Jaya, H. Li Ol57:H7 and gend 3:GN00154	AH0110 probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain C092) C; Species: Yersinia pestis C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 C; Accession: AH0110 R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G il, M.; Mtherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11886360 A;Accession: AH0110 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-658 exime
Query Match 12.5%; Score 373.5; DB 2; Length 1588; Best Local Similarity 23.1%; Pred. No. 2.2e-11; Matches 176; Conservative 95; Mismatches 261; Indels 231; Gap	Gaps 30;	A;Cross_references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175 C;Genetics: A;Gene: YP00902
QY 7 IIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 6 ::	5 926	8; Score 341.5; DB 2; Length 658; 8; Pred. No. 38-10; Tadala 160. Cana 24
OY 61 ESVORSVVGSIQASMEGGGELETISLSMTNDSKEFVDPYIVVTLKAGDNLK 1	< 111 2 976	ATVQANATDEDEBEBLESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIV- 101
Qy 112 IKQNTNENTNASSETYSLKKDLTGLINVE-TEKLSEGANGKKVNIISDTK 1 :	( 160 )	102 -VTLKAGDNLKIKQNT
161 GLNFAKETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDV :  :	7 216 3 1090	DD 150 FALVVSGDNGVGLGNI-TITETTT ALVGARAIGGIAIGGIAIGG 202  QY 156 ISDTKGLNFAKETAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKD 215  1                   1   1   1   1   1
QY 217 LNAG-WNIKGVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIG 2	3 275	מינים מוצגועים שלכתשתתמטער בסקיינים איניים מיניים מינים מיניים מינים מיניים מינים מיניים מיניים מיניים מינים מיניים מיניים מיניים מיניים מיניים מיניים מיניים מיניי

----ISTSMINDSK

----GVNSVALGAGSMASE

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-----SKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQ 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 QVTGSSVASA-SGKESTAIGSGAQAVADNTVAFGGRAIANAVGASALGFDSHAKGI----
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                                                                                                                                                                                                                                                                                                                                                                                             -DIKGLNFAKETAGINGDITVHLNGIGST----LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 TLAGSSASHVDAGNQSTHY---TRAASIKDVLNAGWNIKGVKTGSTTGQSENVDFVRTYD
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                                                                                                                                                                                                                                                                                                                AFAPNAIAL - - - GYNSSVTQSANNGVALGSNSTVS - -
                                                                                                     EEEELESVQRSVVGSIQASME-----GSG-ELET
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Similarity 22.0%; Pred. No. 2e-05;
59; Conservative 102; Mismatches 2
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A; Residues: 1-1325 -BLAT>
A; Cross-references: GB:AE000248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PID:g17877
A; Cross-references: GB:AE000248; GB:U00096; NID:g1787783; PIDN:AAC74583.1; PID:g17877
A; Experimental source: strain K-12, substrain MG1655
A; Experimental source: strain K-12, substrain MG1655
Biochim. Biophys. Acta 1153, 345-347, 1993
A; Title: An Escherichia coli gene showing a potential ancestral relationship to the g
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Cipace: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001
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Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: A64905
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                                                                                                                                                                                                                                                                                                            26;
             A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 689-883, K', 885-1316, 'S', 1318-1325 <RES>
A;Residues: EMBL:X73395; NID:g312392; PIDN:CAA51730.1; PID:g312393
A;Note: the difference in length is due to a frameshift error at pos 653
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTE------VKIGAKTSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282 KEKDGK-LVTGK-----GKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN----NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392 VITNLGTNLGYDGHGEMNISNQGLVVSNGGSSLGYGETGVGNVSITTGGMWEVNKNVYTT
                                                                                                                                           A;Gene: ydeK
C;Function:
C;Function:
C;Feyeription: probably involved in protein translocation apparatus
C;Keywords: nucleotide binding; P-loop
F;712-719/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                        Length 1325;
                                                                                                                                                                                                                                                                                                                                                                    ||:|||:||| | : | |||| | : | ||:
MNRIYRVIWNCTLQVFQACSELTRRAGKTSTVNLRKSSGLTTKFS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      542 MAIGGGTYRGEAGYAI-----GYSSISDGGNWIIKGTASGNSR 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         554
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4.4e-05;
                                                                                                                                                                                                                                                                        8.3%; Score 248.5; 1
23.7%; Pred. No. 4.4e
tive 71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----RLTLGVLLAL---SGSASGASLEVDND----
Reference number: I52440; MUID:94100243
                                                                                                                                                                                                                                                                                             Best Local Similarity 23.7%
Matches 153; Conservative
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 i A;Reference number: A99629; MUD:21156231; PMID:11258796
A;Accession: E90893
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1343 <HAY>
A;Cross-references: GB:BA00007; PIDN:BAB35540.1; PID:g13361583; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics: A;Gene: ECs2117
                                                                                                                                                                                                                                                                               26;
                                                                                                                                                                                                                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---NGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHY----TRAASIKDVLNAGWNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNV - - - - - ESKDNGKRTEVKIGAKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 WLIKNNDSSIEFQIGNQGTGEATIREGGLITAENTIIGGNATG----VGTLNVQ--DQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----KGTTATVSKDDQGNITVMYDVNVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 VITVRRLYNGYFGNGAVNISNNGLINNKEYSLVGVQDGSHGVVNVTDKGHWNFL---GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN-----NIEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNV-----GSKDANKPVRITNVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395 NLGTNLGYDGHGEMNISNEGLVVSNGGSSLGYGETGVGKVSITTGGIWEVNKNVYTTIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP--GKSMMAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGT-----
                                                                                                                                                                                                                                                                                                                     1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL
                                                                                                                                                                                                                                                                               153;
                                                                                                                                                                                                                                        Length 1343;
                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                           81; Mismatches 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              545 GGGTYRGEAGYAI-----GYSSISDGGNWIIKGTASGNSR
                                                                                                                                                                                                                                        Score 231.5; DB 2
Pred. No. 0.00033;
                                                                                                                                                                                                                                                                                                                                                                                                                            ----RLTLGVLLAL---SGSVSGASLEVDNG-----
                                                                                                                                                                                                                                        7.78; 22.98;
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                                                                                                                                                                                                                                        Query Match
Best Local Similarity 22.99
Matches 147; Conservative
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37;

Indels 183; Length 1238;

19 VSELTRNHT-----KRASATVKTAVLATLLFAT--VQANAT-----DEDEEEELESVQR

SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENTNASSF

99

TYSLKKDLTGLINVETEKLSF - - GANGKKVNIISDTKGLNFAKETAGT - - NGDTTVHLNG

126

:| :| | : | | : | | 241 VGGVITDI-----NID-GDISSANSQAARIYNYTNGGLASLRFRANNVTGSTGLYIDN 292

IGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTG-----

182

QSEN---VDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIK-----E 283

350

335 407 390

QADKFETVTSGTNVTFASGKGTTATVSKDDQGNITVMYDVNVGDA---LNVNQL--QNSG 

284 KDGKL-----VTGKGKGENGSSTD----EGEGLVTAKEVIDAVNKAGWRMKTTTANGQTG 334

293 SSONGAVTDIILTGD---LTATSGSALQANAYSDEGNIETAIKLNNVYSLYDALNISDYT

454 444 505 ----GAGADAPTLSVD--DEGAL-----NVGSKDANKP

POFSSVSL----

445 909 480 VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYL---

WNLDSKAVAGSSGK--VISGNVSPSKGKMDETVNINAGNNIEISRNGK---NIDIATSMA

614 SYAEINDAALDLANSHLVLGGA---GDAAFDLTRIDNREEAILDGDPNRITGFGTLTKTN 670

N--WIIKGT--ASGNSRGHFGASASVG 589 671 NSIWTLTGANMADGDANAFLSANIAGG 697

267

---PGKSMMAIGGGTYRGEAGYAI---

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A;Residues: 1-1238 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89171.1; PID:g15978410; GSPDB:GN00175 C;Genetics: A;Gene: YP00309
                                                                                                                                 Ouery Match 7.4%; Score 220.5; DB 2; Best Local Similarity 20.7%; Pred. No. 0.0011; Matches 142; Conservative 123; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ω
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C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Species: Versinia Postis
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
I, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, R.W.; Multehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0038
A;Status: preliminary
A;Molecule type: DNA
                             A.Molecule type: DNA
A;Residues: 1-1343 <STO>
A;Residues: 1-1343 <STO>
A;Residues: 1-1343 <STO>
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ydeK
                                                                                                                                                                                                                                                   27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVIKEKDGKLVTGKGKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTGQADK 338
                                                                                                                                                                                                                                                                                                                                                                             61 ESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHY----TRAASIKDVLNAGWNIK 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNV-----ESKDNGKRTEVKIGAKT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 VITVRRLYNGYFGNGAVNISNNGLINNKEYSLVGVQDGSHGVVNVTDKGHWNFLGTGEAF 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 --VNVGDA----LNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNN 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         347 RYIYIGDAGXGELNVSR----EGKVDSGIITAGMKETGTGNLTV---KDKNSVITNLGTN 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 IEISRNGK-NIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNV-----GSKDANKPVR 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 LGYDGHGEMNI-----SNEGLVVSNGGSSLGYGETGVGKVSITTGGIWEVNKNVY 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 ITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLVQAYLP--GK 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 450 TTIGVAGVGNLNISDGG--KFVSQNITFLGDKASGIGTLNLMDATSSFDTVGINVGNFGS 507
                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                           1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : : | : | :: | | | :: | | | DVAYDAYLVGWYGTGVLNILA----GGNASLTTITTSVIGGN--EDSEGTVNVLGGTWR
                                                                                                                                                                                                                                                                                                                                                                                                             ----RLTLGVLLAL---SGSVSGASLEVDNG------QITNIDT
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                                                                                                                                                                                                                                                   Indels 163;
                                                                                                                                                                                                      Length 1343;
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                                                                                                                                                                                                                                                                                                                   1 MNRIYRVIWNCTLQVFQACSELTRRVGKTSTVNLRKSSGLTTKFS----
                                                                                                                                                                                                      7.6%; Score 227.5; DB 2; 22.7%; Pred. No. 0.00053; tive 86; Mismatches 252;
                                                                                                                                                                                                      Query Match
Best Local Similarity 22.78
Matches 147; Conservative
             Status: preliminary
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                                                       Aida-I adhesin-like protein [imported] - Escherichia coli (strain 0157:H7, substrain C; Species: Escherichia coli C; Species: Escherichia coli C; Species: Bscherichia coli C; Species: 18-0ul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C; Accession: D90803 R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. A; Reference number: 8, 11-22, 2001 A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and g A; Reference number: A99629; MUID:21156231; PMID:11258796 A; Accession: D90803 A; Status: preliminary A; Molecule type: DNA
15
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42; A;Cross-references: GB:BA000007; PIDN:BAB34819.1; PID:g13360856; GSPDB:GN00154 A;Experimental source: strain 0157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: EC81396 STATELIAG--GDOSVH----GRALNTTLNG-------GRQYVHRDGLA-LNTVINEGGW 276 277 QV--VKAGGAAG------308 EGSGELET-----LKAGDNL 110 111 KIKQNTNENTNA----SSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFA 165 231 KEKDGKLVT-----315 309 ONTGCALVISTAATVIGTNRLGNFTVENGKADGVVLESGGRLDVLESHSAQNTLVDDGGT 368 484 422 423 -----NAGN-NIEISRNGKNIDI-----ATSMAPQFS-SVSLGAGADAPTLSVDD 465 604 : : : : : : : DEDWYLRSENAYRAEVPLYTSMLTQAMDYDRILAGSRSHQTGVNGENNSVRLSIQGGHLG 664 KET---AGINGDITVHLNGIGSTLIDILAGSSASHVDAGNQSTHYTRAASIKDVLN-AGW 221 NIKGVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVI 281 316 -AVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGK--------GTT 357 -----VNVGDALNVNQLQN 387 Gaps -----QASM 75 1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVK-----TAVLATLLFATVQANATDE 54 545 IGKTWLAFTNVGNSNLGVATTGQGIRVVDAQNGATTEEGAFALSRPLQAGAFNYTLNRDS 183 -LATGIINTGAEGGPDSDNSYTGQK-----VQGTAESTIINKNGRQIILFS-----GLA EGALNVGSKDANK --- PVRITNVAPG -----VKEGDVTNVAQLKGVAQNLNNRI-----665 HDNNGGIARGAIPESSGSYGFVRLEGDLLRTEVAGMSLTTGVYGAAGHSSVDVKDDDGSR 388 SGWNLD----SKAVAGSSG-----KVISGNVSPSKGKMDETVNI-----SKAVAGSSG-----GCTYRGEAGYAIGYSSI--SDGGNW---IIKGT----ASGNSRGHFGASASVGYQW 592 Indels 307; 7.3%; Score 219.5; DB 2; Length 949; 21.4%; Pred. No. 0.00087; Live 97; Mismatches 253; Indels 307 512 -DNVDGNARAGIAQAIATAG-----LVQAYLPGKSMM-----AIG---EEEELESVORSVVGSI-ATVSKDDQ-GNITVMYD----Similarity 21.4 79; Conservative A; Residues: 1-949 <HAY> Query Match Best Local Simi Matches 179; -22 232 358 485 92 166 466 605 ò g õ qq à Q δ ద ö qq ò g ò g δ g ŏ g ò q ò g ò g ò g ŏ

Search completed: July 3, 2002, 08:38:38 Job time: 309 sec

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Mon Juî

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 3, 2002, 08:49:07; Search time 29.79 Seconds (without alignments) 769.452 Million cell updates/sec Run a:

US-09-771-382-10 2988 1 MNKIYRIIWNSALNAWVAVS......TASGNSRGHFGASASVGYQW 592 Tite: Pefect score: Squence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

105224 seqs, 38719550 residues Searched:

105224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		-	P15320 serratia ma	Q9kka3 r outer mem	P39180 escherichia	Q53047 r outer mem		P25927 salmonella		P35828 caulobacter	P96989 r outer mem	O06653 r outer mem	P38536 t amylopull	es		. P35827 campylobact		009624 caenorhabdi	Q02629 saccharomyc	P34487 caenorhabdi	_	Q07833 bacillus su	P14914 rickettsia			_		-	P49051 bacillus an	P06620 pseudomonas		46113	P44969 haemophilus
SUMMARIES	ID	YDEK	AIDA_ECOLI	HLYA_SERMA	OMPB_RICCN	AG43_ECOLI	OMPB_RICRI	ICEN_XANCT	BIGA_SALTY	OMPA_RICRI	SLAP_CAUCR	OMPB_RICTY	OMPB_RICJA	APU_THETU	YDBA_ECOLI	OMPA_RICCN	SLAP_CAMFE	HLYA_PROMI	YS89_CAEEL	N100_YEAST	YMJB_CAEEL	ICEV_PSESX	WAPA_BACSU	120K_RICRI	ICEN_PANAN	ICEA_PANAN	YPJA_ECOLI	ICEN_PSEFL	ICEN_ERWHE	SLA1_BACAN	ICEN_PSESY	OMPB_RICPR	FLA3_CAMJE	IGAO_HAEIN
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P45384 haemophilus Q08860 shigella fl	P22251 campylobact 084419 chlamydia t	O30611 pseudomonas	Q46114 campylobact	P12021 sus scrofa	P22252 campylobact	P50493 plasmodium	P04949 escherichia	P35825 bacillus st	Q9z812 chlamydia p
IGA2_HAEIN FLIC_SHIFL	FLA2_CAMJE PMPC_CHLTR	ICEK_PSESX	FLB3_CAMJE	APMU_PIG	FLB2_CAMJE	PVDB_PLAKN	FLIC_ECOLI	SLAP_BACST	PM20_CHLPN
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162 161	161 161	160	159.5	159	158	157.5	156	156	155
34 35	36 37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                 Adhesin aidA-I precursor.
                                                                      Escherichia coli.
                                                                                                                       NCBI_TaxID=562;
                                                                                     Plasmid pIB6
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           (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                            1 HISTHISTOLINGTLOVEQACSELTRRAGKTSTVNLRKSSGLTTKFS--------
                                                                                                                                                                                                                                                                                      159;
                                                                                                                                                                                                                                                              Length 1325;
                                                                                                                                                            POTENTIAL.

HYPOTHETICAL LIPOPROTEIN YDEK.

N-ACYL DIGLYCRRIDE (POTENTIAL).

N -> K (IN REF. 3).

M -> S (IN REF. 3).

M-S (IN REF. 3).

M-S (AN REF. 3).
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                                                                                                PIR; S34315; S34315.
ScoGene; BG11780; ydeK.
PROSITE: PS00013; PROMAR LIPOPROTEIN; 1.
Hypothetical protein; Membrane; Lipoprotein; Signal;
                                                                                                                                                                                                                                                           8.3%; Score 248.5; DB 1;
23.7%; Pred. No. 2.9e-05;
ive 71; Mismatches 263;
                                                                                                                                                                                                                                                                                                                                                                                       ----RLTLGVLLAL---SGSASGASLEVDND-----
 modified and this statement is not removed.
            entities requires a license agreement (or send an email to license@lsb-sib.ch)
                                                            EMBL; D90793; BAA15190.1; ALT_INIT.
EMBL; D90794; BAA15197.1; ALT_INIT.
EMBL; X73295; CAA51730.1; ALT_FRAME
                                                  EMBL; AE000248; AAC74583.1; -.
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Best Local Similarity 23.7%
Matches 153; Conservative
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                                                                                                                                                                      -----ISDTKGLNFAKE----TAGTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGN
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SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
STRAIN=2787 (0126:H27);
MEDILINE-92326638; PubMed=1625582;
Benz I., Schmidt M.A. involved in diffuse adherence of the diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132271 MW; B2A00F72AC05FB34 CRC64;
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PIR; S28634; S28634.
Cell adhesion; Signal; Outer membrane; Plasmid.
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PRT; 1286 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
                   402
                                                    442
                                                                                    447
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Poole K., Schiebel E., Braun V.;
Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 RNHTKRASATVKTA----VLAT-----LLFATVQAN-----ATD-----EDEEEEL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
                   -- DSKAVAGSSG
                                                  390 LSDGYARGTILNNSGRENVS-----NGGVSYNAMINTGGNQYIYSDGEATAAIVNTSG
                                                                                      --DIATSMAPOF
                                                                                                                 443 FORINSGGTAPVONSVVVTRTVSSAAKPFDAEVYSGGKQTVYLWRGIWYSNFLTAVWSMF
                                                                                                                                                                               VRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARA-----GIAQAIATAGLVQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.6%; Score 197; DB 1; Length 1608;
21.8%; Pred. No. 0.013;
ive 82; Mismatches 255; Indels 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
                                                                                    --KVISGNVSPSKGKMDETVNINAGN---NIEISRNGKNI----
                   FASGRGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Outer membrane. SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        1608 AA
                                                                                                                                                                                                                                                                                                                   | :: | | | | :: | :| | | | 601 --TGINIK--NGGIIRVDSGASALNIALSSGGN 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A28182; A28182.
Hemolysis; Toxin; Outer membrane; Signal.
                                                                                                                                                                                                                                                                                               535 YLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HEMOLYSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SN8;
MEDLINE=88257037; PubMed=3290200;
Poole K., Schiebel E., Braun V.;
                                                                                                                                                         SSVSLGAGADAPTLSVDDEGALN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M22618; AAA50323.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hemolysin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       marcescens.
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P15320;
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 41, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Scas) (rompa) (romp B) (Contains: 120 kDa surface-exposed protein (Surface protein)
antigen) (120 kDa outer membrane protein omp8); 32 kDa beta peptide].
                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                           609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: :|| | | : || ASGGELSVESKTGNINVK------AAERQONIDEQKTALTVNGYAKEAGDKQYRAGL 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNGKNIDIATSMAPQFSSVSL----GAGADAPTLSVDDEG------ALNV 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --INARDKLTQQGAQHSVGGAYQENAAGVDHLAAADTASTTTTKTD--VGVNIGANVDYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLN-------NRIDNVDGNARAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSIDIN-----AKGEVRDQGTQYQASKG-AVNLTADSHRSEAAANRQDEQSRDTR--
                                                                                                                                                                                                                                                                                                           RGYORNHTSSLRTGRWSNSDESESLKASELRSEGE-----LTLKAGRNVSTOGAKVHA
                                                                                                                                     ------KIKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANG---KKVNIIS
                                                                                                                                                                                                         ------VRDDKTSWGGIGGGDNKNN--S
                                                                                                                                                                                                                                                                              DTKGLNFAKETAGTNGDTTVHLNG-IGSTLTDTLA-GSSASHVDAGNQSTHYTRAASIK-
                                                                                                                                                                                                                                                                                                                                                                                                                DVLNAGWNIKGVKTGST---TGQSENVDFVRTYDTVEFLSADTKTTVNVESKD-NGKRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----EVKIGAKTSVIKEKDGKLVTGKGKGENGSSTDEGEGLVT----AKEVIDAVNKAGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIEHTRDSEKTTRTENSASSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGNKVSFLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 KGTTA-----TVSKDDQGNITVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 YDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGNNIEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 IAQAIATAGLVQAYLPGKSMMAIG----GGTYRGEAGYAIGYSSISDGGNW------
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Rickettsiaceae; Rickettsieae; Rickettsia.
ESVQRSVVGSIQAS-MEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1655 AA
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                 Stenos J., Walker D.;
Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia
australis, the most divergent rickettsia of the spotted fever group.";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 KDA BETA PEPTIDE.
P -> A (IN STRAIN INDIAN TICK TYPHUS).
G -> S (IN STRAIN INDIAN TICK TYPHUS).
K -> N (IN STRAIN INDIAN TICK TYPHUS).
V -> A (IN STRAIN INDIAN TICK TYPHUS).
N -> D (IN STRAIN INDIAN TICK TYPHUS).
I -> V (IN STRAIN INDIAN TICK TYPHUS).
R -> I (IN STRAIN INDIAN TICK TYPHUS).
R -> L (IN STRAIN INDIAN TICK TYPHUS).
R -> L (IN STRAIN INDIAN TICK TYPHUS).
                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: CELL WALL, THIS BACTERIUM IS COVERED BY A S-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----NGKVATIDGQV 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 ATVQANATDEDE-----EEELESVQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPY 99
                                                                                                                                                                                                                                                                                                             FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                  "Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB)."; Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
                         "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 ATITFNGTDGTGRLVLLSKNAAATDFNVTGSLGGNLKGIIEFNTVAVNGQ-----
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDA SURFACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1655;
                                                                                                                                                                                                                                                                                                                                                     LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
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E -> D (IN REF. 3).
G -> S (IN REF. 3).
H -> R (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.6%; Score 197; 22.4%; Pred. No. 0
                                                                               Malish 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell wall; complete
                                                                               STRAIN∾Indian tick typhus, and Mal
MEDLINE=20393643; PubMed=10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF123721; AAF34124.1; -. EMBL; AF123726; AAF34129.1; -.
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SEQUENCE OF 353-1655 FROM N.A.
                                                                  SEQUENCE OF 33-1649 FROM N.A.
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11177
1492
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75
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                                                                                                           Roux V., Raoult D.;
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1177
1492
1655
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                                                                                                                                                                                          STRAIN-Malish
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              Raoult D.;
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Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori H., Mori H., Moroura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T., A., A. (60-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                            351 YAKDMVIQSANAVGQVNFRHIVDVGTDGTTAFKTAASKVAITQNSNFGTTDFGNLAAQII 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              264 KDNG-----KRTEVKIGAKTSVIKEKDGKLVTGK------GKGENGSSTDEGEGLV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                      TAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVT-----SGTNVTFASGKGTTAT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12 / MG1655,
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       576 TS--TQNNIVVDEDLAIATDQTGVVDASSLTNAQTLTINGKIGTVGANNKTLGQFNIGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     694 LGS-ATNPLAEINFGSKGAANVDTVLNVGKGVNL-YATNITTTDA---NVGSFIFNAGGT
160 KGLNFAKETAGTNGDTT----VHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAAS---
                                                                                                                                           IKDVLNAGWNIKG - - VKTGSTTGQSENVDFVRTYD - - - TVEFLSADTKTTTVN - - - - VES
                                                                                                                                                                                                                                                                                                                                                               464 SGAGVVQLSGTHAAELRLGNAGSVFKLADGTVINGKVNQTALVGGALAAGTITLDGSATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 VSKDDQGNITVMYDV-----NVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGKM-DETVNIN---AGNN--IEISRNGKNIDIATSMAPQ-----FSSV----SLGAGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NARAGIAQAIATAGLVQ-----AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 APTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ol-wov-1997 (Rel. 35, Last sequence update) 16-0CT-2001 (Rel. 40, Last amnotation update) Antigen 43 precursor (AG43) (Fluffing protein). FLU OR B2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1039 AA
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P39180; P76360; P75614; P97241; Q46771;
O1-FEB-1995 (Rel. 31, Created)
01-NOV-1997 (Rel. 35, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
MEDLINE=97251358; PubMed=9097040;
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27;

Gaps

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355 354 572

us-09-771-382-10.std.rsp

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85 ISTGLEYGPDNEA-----NTGGQWV-----ODGGTANKTTVTSG 118
                                                                                                                                                                                                                                                                                                                                                                                                                      356 TTATVSKDDQCNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSK-- 413
                                                                                                                                                                                                                                                                                                                                       121 NASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                511 AVNL---NEGTLTLNDSTVTTDVIAQRGTALKLTGSTVLNGAIDPTNVTLASGATWNIPD 567
                                                                                                                                                                                                                                                                            61 ESVQRSVVGSIQASMEGSGELETISLSMINDSKEFVDPYIVVTLKAGDNLKIKQNTNENT 120
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) (Contains: 120 kDa surface-exposed protein (Surface protein)
                                                                                                                                                                                                               1 MNKIYRIIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL 60
                                                                                                                                                                                                                                            5 LNTCYRLVWNHMTGAFVVASELARARGKRGGVAVALSLAAVTSLPVLAADIVVHPGE--- 61
                                                                                                                                                                                                                                                                                                                                                                                                   GI-----GSTLTDTL--AGSSAS-----HVDAGNQSTHYTRAASIKDVLNAGWNIKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 VKPGTVATDTVVNTGAEGEPD-AENGDTGQFVRGDAVRTTINKNGRQIVRAEGTANTTVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTAKEVIDAVN---KAGWRMKTTTANCQTG--QADKFETVT-SGTNVTFASG-----KG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---GKMDETVNINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          471 VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            462 LSGKTVN-----NDTLTIREGD----ALLQGGSLTGNGSVEK-SGSGTLTVSNTTLTQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     531 LVQAYLPGKSMMAIGGGT----YRGEAGYAIGYS-----SISDGGNWIIKG
                                                                                                                                                                                                                                                                                                        -----TLANHDNQIVFGTTNGMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 VKTGS-----TTGQSENVDFVRTYDTVEFLSADTKTTTVN-----VESKDNGKRTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 KIGAKTSV------IKEKDGKLVTGKGKGENGSSTDEGEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 HTATNIRVDDGG---TLDVRNGGTATIVSMGNGG----VLLADSGAAVSGTRSDGKAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          406 SIGGGOADALMLEKGSSFTLNAG----DTATDTTVNGGLFTARGGTLAGTTTLNNGAILT
LNLVHTS -> MNLIYNA (IN STRAIN ML 308-
                                                                                                                                                    6.6%; Score 196.5; DB 1; Length 1039; 20.1%; Pred. No. 0.0083; tive 79; Mismatches 268; Indels 185;
                                         S -> T (IN STRAIN ML 308-225).

O -> L (IN STRAIN ML 308-225).

S -> I (IN STRAIN ML 308-225).

ETV -> TTT (IN REF. 5).

MW, 5170D647C8DEEBE0 CRC64;
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                               OGT ->
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Q53047;
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CONFLICT
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                                                                                                                                                                    "Purification and N-terminal sequence of the alpha subunit of antigen 43, a unique protein complex associated with the outer membrane of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEMS Microbiol. Lett. 149:115-120(1997).
                                                                                                                                                                                                                                                                                             Link A.J., Robison K., Church G.M.; "Comparing the predicted and observed properties of proteins encoded in the genome of Escherichia coli K-12."; Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                      Henderson I.R., Meehan M., Owen P.;
"Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION AS AN ADHESIN.
SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             I (IN STRAIN ML 308-225).
N STRAIN ML 308-225).
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SL -> FF (IN STRAIN ML 308-225).

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ATN -> STI (IN STRAIN ML 308-225).

ATN -> STI (IN STRAIN ML 308-225).

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S -> N (IN STRAIN ML 308-225).

E -> Y (IN STRAIN ML 308-225).

H -> Y (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).

GHL -> SHF (IN STRAIN ML 308-225).

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C -> S (IN STRAIN ML 308-225).

C -> S (IN STRAIN ML 308-225).
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-i- SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETELLA PERTACTIN.
                                                            Henderson I.R., Owen P.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTIGEN 43 ALPHA CHAIN. ANTIGEN 43 BETA CHAIN.
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SIGNAL 1 52
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                                                                                                                                                                                                                                                               STRAIN-K12 / EMG2;
MEDLINE-97443975; PubMed-9298646;
                                                                                                                                       MEDLINE=89291704; PubMed=2661530;
Caffrey P., Owen P.;
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97257509; PubMed=9103983;
                                                                                                         PRELIMINARY SEQUENCE OF 53-78.
 DNA Res. 3:379-392(1996)
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                               SEQUENCE FROM N.A. STRAIN=ML 308-225;
                                                                                                                          STRAIN=ML 308-225;
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570 IKGTASGNSRG 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39;
                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
-!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 EEELESVQR-----SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDN 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 TGRLVLLSKHAAATNFNITGSLGGNLKGVIEFNTVAV----DGQ------LTANAGAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110 LKIKQNTNENTNASSFTYSLKKDLIGLINVETEKLSFGANGKKVNIISDTKGLNFAKETA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 A----ITLIGNETGDASNPGNTAGVITFDANGTLESASADANVAVTNNITAIEASGAGV 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 NGFIQVS-----NKSFATVKAINIADGQGIIFNTDANNANTLNLQAGGTTINFTGTDG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NGKVATIDGQVYAKDMVIQSA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 NATGOVNFRHIVDVGADGTTAFKTAASKVTITQDSNFGNTDFGN-----LAAQIK-VPN 413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 181; Gaps
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]
                                                                                                                                                                                                                                                                                                Gilmore R.D. Jr., Joste N., McDonald G.A.;
"Cloning, expression and sequence analysis of the gene encoding the
"Cloning, expression and sequence analysis of the gene encoding the
120 kD surface-exposed protein of Rickettsia rickettsii.";
Mol. Microbiol. 3:1579-1586(1989).
-!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---VQA----NATDEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 GTNGDTT----VHLNGIGSTLTDTLAG-----SSASHVDAGNQSTHYTRAASIKDVLN
                                                                                                                                      MEDIINE=92167802; PubMed=1724278; Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.; "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 AGWNIKGVKTGSTTGQSE---NVDFVRTYD---TVEFLSADTKTTTVN----VESKDNG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 KDA SURFACE-EXPOSED PROTEIN.
                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                      evidence for protein processing from a large precursor.";
Mol. Microbiol. 5:2361-2370(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.5%; Score 194.5; DB 1;
23.5%; Pred. No. 0.018;
tive 89; Mismatches 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 KDA BETA PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 NAWVAVSELTRNHTKRASATVKTAVLAT - - LLFAT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       319 NAVIGTNNGAGRAAGFVVSVD-----
                                                                                                                                                                                                                                                                                     MEDLINE=90136087; PubMed=2515418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB: 1.
Antigen; S-layer; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1181 1188 POI
1654 AA; 168184 MW;
                                                                                                                                                                                                                                                      SEQUENCE OF 279-1654 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X16353; CAA34403.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                               Rickettsia rickettsii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 158; Conserv
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1334
                                                                                NCBI_TaxID=783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                GNITVMYDV------NVGDALNVNQLQNSGWN-----LDSKAVA----GSSGKVIS- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNVSPSKGKMDETVNINAGNNIEISRNGKNIDIATSMAPQ----FSSV----SLGAGAD 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THAT OF ICE.
469 VQLSGTHAAELRLGNAGSIFKLADGTVINGKVNQTALVGGALAAGTITLDGSATITGD--
                                                                                                                                                                                                                527 IGNAGGAAALQRITLAN-----DAKKTLTLGGANIIGAGGGTIDLQANGGTIKLT-STQ
                                                                                                                                                                                                                                                                                                                                                                                     580 NNIVVDFDLAIATDQTGVVDASSLTNAQTLTINGKIGTIGANNKTLGQFNIGSSKTVLSN
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Mol. Gen. Genet. 223;163-166(1990).
-!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
                                                                                                                                314 IDAVNKAGWRMKTTTANGQTGQADKFETVT-SGTNVTFASG-----KGTTATVSKDDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 APTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  694 LGS-ATNPLAEINFGSKGVNVDT-VLNVGEGVNL-YATNITTTDA---NVGSFVFNAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 NARAGIAQAIATAGLVQ-----AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRYSTALLIZATION IN SUPERCOOLED WATER.
SUBGELLULAR LOCATION: Outer membrane (By similarity).
DOMAIN: CONTAINS 153
DOMAIN: CONTAINS 154
DOMAIN: CONTAINS 154
CRASHER OF THE CONSENSUS
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
MISCELLANBOOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF IC
SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas campestris (pv. translucens).
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao J., Orser C.S.; "Conserved repetition in the ice nucleation gene inaX from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1567 AA
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HSSP; P06620; IINA.
HTGFPFO; IPR000258; ICe_nucleatn.
Pfam; PF000818; ICe_nucleation; 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91080859; PubMed=2259339;
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             MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latrellle P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                  J. Bacteriol. 173:325-333(1991).
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 414 and 732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102 VILKAGDNLKIKQNTNENTNASSFTYSLKKDLTGLI-----NVET----EKLSFGANGKK 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NATDEDEEEELESVQR-----SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIV 101
                                                                                                                                                                                                           coli NADPH-sulfite reductase:
to overcome limiting stroheme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PUTATIVE SURFACE-EXPOSED VIRULENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 189; DB 1; Length 1953;
Pred. No. 0.042;
93; Mismatches 253; Indels 170;
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A -> R (IN REF. 3).
D -> N (IN REF. 1).
QYLE -> ITLO (IN REF. 1).
SA -> T (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA -> T (IN REF. 1).
W; 611B3F1C954D91AE CRC64;
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15 X 11 AA TANDEM REPEATS.
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2 (INCOMPLETE).
3 (INCOMPLETE).
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                                                                                                                                                                                             Wu J.Y., Siegel L.M., Kredich N.M.;
"High-level expression of Escherichia
requirement for a cloned cysG plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M64606; AAA27042.1; ALT_FRAME.
BMBL; M64606; AAA27043.1; ALT_FRAME.
PIR; C39200; C39200.
PIR; D39200; D39200.
StyGene; SG10437; bigA.
Virulence; Repeat; Signal; Complete
   MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                 MEDLINE-91100301; PubMed=1987123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200150 MW;
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EMBL; AE008859; AAL22340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.98;
                                                                                                                                                 SEQUENCE OF 1-765 FROM N.A.
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e; Repeat; Signal;
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Best Local Similarity 21.9
Matches 145; Conservative
                                                                                                                      Nature 413:852-856(2001).
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1798
1837
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                                                                                                                                                                   STRAIN-LT2;
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CONFLICT
SEQUENCE
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                                                                                                                                                                              760 SDVTAGYGSTGTAGADSTLIAG--YGSTQTSGSD-----SSLTAGYGSTQTARKGS- 808
                                                                                                                                                                                                           ELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENTNASSFTYSLKKDLTGLINV 139
                                                                                                                      Gaps
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                                                                                                                                                 SELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEELESVQRSVVGSIQASMEGSG
                                                                                                                                                                                                                                        ---DITAGYGSTGTAGADS----TLIAGYG-----STQTSGSDSSLT-----AGYGST
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                                                                                                                                                                                                                                                                                                   QTAR----EGSDV----TAGYG----STGTAGADSTLISGYGSTQT---AGSDSS-LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1042 QTARQGSDVTAGYGSTGTAGADSTLIAGYGSTQTAGSDSSLTAGYG-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIGA OR STM3470.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                    Score 189; DB 1; Length 1567;
Pred. No. 0.032;
3; Mismatches 265; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGY----AIGYSSISDGG--NWIIKGTASGNSRGH-----FGASASVGYQ 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIGA_SALTY STANDARD; PRT; 1953 AA.
P25977; P25928; Q9XCQ3;
P1-MAY-1992 (Rel. 22, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Putative surface-exposed virulence protein bigA precursor.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 57.
ICE nucleation; Repeat; Outer membrane.
SEQUENCE 1567 AA: 152548 MW: C8B451D959ECAD63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=14028;
Stojlijkovic I., Valentine P., Heffron F.;
"Salmonella typhimurium rhs homolog.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 700720;
                                                                                                                   83;
                                                                                    6.3%;
                                                                                                                   Matches 128; Conservative
                                                                                                     Similarity
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                                                                                      Query Match
Best Local 3
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32;

Gaps

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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                              ---SVSGDSNAVDITGNVN----ISADYGQDDLAAG-APPLTGVVVGGNGNTVTLN-- 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --GALNIDDNDLSATGGQYLDVVGLSVTGDDNDVEIDGGINITHSEDPLDGTSADITGIS 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa antigen) (Cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  779 VSGNSTVTLNGHSTIDTNTVVGGHVVLARVNNGGSLILGDDSVVDVNVSYIPTGYYTYNA
                                                                          ----LAGSSASHVDAGNQSTHYTRAASIKDVLNAGW----NIKGVKTGSTTGQSENVDFV
                                                                                                                                                                                        RTYDTVEFLSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKG-----KG
                                                                                                                                                                                                                    ----TALYIEGDNALVINEGNQTISGGAVGTRIDGDDAHTTNTGDIAVDGAGSAAVIING
                                                                                                                                                                                                                                                          ENGSSTDEGEGLUT -- AKEVI -- DAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTF -
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                                                                                                                                                      SDISGAGSTGTVIDGNNARVNNDGDMTITDGGTGGHITGDNVVIDNAGSTTVSGADA---
                                                     --NFAKETAGINGDITVHLNGIGSTLTDT--
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PTM: CLYCOSLATED (PROBABLE).
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 QNLNNRI-----DNVDGNARAG----IAQAIATAGLV----
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(Rel. 14, Last sequence update)
(Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeated, near identical sequences.";
Infect. Immun. 58:2760-2769(1990).
-!- FUNCTION: ELICITS PROTECTIVE IMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90354033; PubMed=2117568;
                                                   V----TKGL----
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to licenseélsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LESVQRSVVGSIQASMEG-----SGELETISLSMTNDSKEFVDPYIVVTLKAG--- 107
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A (TYPE I).
B (TYPE II).
C (TYPE II).
C (TYPE II).
F (TYPE II).
G (TYPE II).
G (TYPE II).
K (TYPE I).
I (TYPE II).
M (TYPE II).
M (TYPE II).
M (TYPE II).
TYPE I (INCOMPLETE).
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                                                                                                                                                                      wall; S-layer; Glycoprotein
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; Pred. No. 0.052;
79; Mismatches 2
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InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
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SIGNAL
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506
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SEQUENCE FROM N.A.

SERAIN-ATCC 19089 / CB15;

MEDLINB-21173698; pubMed=11259647;

MEDLINB-21173698; pubMed=11259647;

Micrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

"Complete genome sequence of Caulobacter crescentus.";
A S-
                                                                       1264 SVGDVTILN----AQNINFRARDSVLVLSNLTG---VGVNNILLAADLV---APGADEG 1312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025. STAIN-WATC 19089 / CB15; MEDLINE-93007489; Pubmed-1393820; Gilchrist A., Fisher J.A., Smit J.K.; Mucleotide sequence analysis of the gene encoding the Caulobacter crescentus paracrystalline surface layer protein."; Can. J. Microbiol. 38:193-202(1992).
                                             490 KEGDVTNVAQLKGVAQNLNNR-----IDNVDGNARAGIAQAIATAGLVQAYLPG--KS
                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Caulobacter group,
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                                                                                                                                                                                                                                                    16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
S-layer protein (Paracrystalline surface layer protein).
RSAA OR CC1007.
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20 STRAIN-ATCC 19089 / CB15;
                                                                                                                                                                                                                  PRT; 1025 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-89008089; Pubmed-3049545;
Fisher J.A., Smit J.K., Agabian N.;
"Transcriptional analysis of the major
                                                                                                                                      1313 TVVFNGGVNGLNVGSNVAGTARNIGDGG 1340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REVISIONS TO 376; 636 AND 842-843.
                                                                                                         541 MMAIGGGTYRGEAGYAIGYS--SISDGG
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P35828 046015;
01-UJN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 AALIGTILNAATVSGIGGYATATAAMIND---LSDGALSTDNAAGVNL---FTAYPSSGV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSFTYSL---KKDLTGLINVET-------EKLSFGANGKKVNIISDTKGLNF 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 VQAAAVTALPTGVTISGIETMNVTSGAAITLNTSSGVTGLTALNTNTSGAAQTVTAGAGQ 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STHYTRAASIKD--VLNAGWNIKGVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNV 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESKDNGKRTEVKIGAKTSVIKEKDGKLVTGKGKGENGSSTDEGEGLVTA-KEVIDAVNKA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAVTGGTAVTVAQTAGNAVNTTLTQADVTVTGNSSTTAVTVTQTAAATAGATVAGRVNGA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GWRMKTTTANGQTGQADKFETVTSG------TNVTFASGKGTTATVSKDDQGNI 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVMYDVNVGDALNVNQLQNSGWNLDSKAVAGS-----SGKVISGNVSPSKGKMDETVN 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73; Mismatches 274; Indels 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1025;
                                                                                                                                                                                                                                                                                                                                               Cell wall; S-layer; Calcium-binding; Complete proteome. INIT_MET 0 \ 0
                                                                                                                                                                                                                                                                                                                                                                                     98001 MW; AD7A326E1363D8AC CRC64;
                    SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              6.3%; Score 187; DB 1; 24.1%; Pred. No. 0.024;
                                                                                                                                                                                                                                                                                       InterPro; IPR001343; Hemlysn_Ca_bind.
Pfam; PF00353; hemolysinCabind; 1.
PRINTS; PR00313; CABNDNGRPT.
                                                                                                                                                                                                                                   AAK22991.1; ALT_INIT
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                                                                                                                                                                                                               EMBL; AF062345; AAC38665.2; -
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                                                                                                                                                                                                                                                     HSSP; P01549; 2MCM.
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                                                                                                                                                                                                                                                                     CC1007
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Best Local S
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANCHOR.
                                                                                                                                                                                                                                                   MEDLINE=94040787; PubMed=8224886;
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
"Cloning and sequence analysis of the gene encoding the crystalline
surface layer protein of Rickettsia typhi.";
Gene 133:129-133(1993).
                                                                                                                                                                                                                                                                                                                                                                                   Ching W.M., Carl M., Dasch G.A.; "Mapping of monoclonal antibody binding sites on CNBr fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-LAYER WITH HEXAGONAL SYMMETRY.
SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEMBRANE ANCHOR (POTENTIAL)
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V -> I (IN REF. 2).
G -> A (IN REF. 2).
G -> S (IN REF. 2).
           1645 AA
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                                                                                                                                                                                   Rickettsiaceae; Rickettsieae; Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                      PubMed=1370573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      iDENTIFICATION OF CLEAVAGE SITE. MEDLINE=92104668; Pubmed=1729180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003858; rOmpA_rOmpB.
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           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92114896;
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                                                                                                                                                       Rickettsia typhi.
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             OMPB_RICTY
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                                                                                                                                                              ELET --- ISLSMINDSKEFVDPYIVVTLKAGDNLKIKQNINENINASSFTYSLKKDLTGL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSKAVAGSSGKVISGNVSPS-----KGKMDETVNI-------NAGNNIEISR 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 NGKNIDIATSMAPQFSSVSLGAGA---DAPTLSVDD--EGALNVGSKD---ANKPVRITN 484
                                                                                                                                                                                       155 VSKVNAGAAINDNDLSGVGSIDFTAAPSVLEFNLINPTTQEAPLTLGDNAKIVNGANGIL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NITNGFVKVSDKTFAGIKT-INIGDNQGLMFNTTPDAANALNLQGGGNTINFNGRDGTGK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 LVLVSKNGNATEFNVTGSLGGNLKGVIEFDTTAAAGKLIANGGAANAVIGTDNGAGRAAG 333
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30-MAY-2000 (Rel. 39, Last Sequence update)
30-MAY-2000 (Rel. 39, Last anoutation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 kDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sosa) (Tompp)
(rOmp D) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompb); 32 kDa beta peptide).
                                        Gaps
                                                                                28 KRASATVKTAVLATL-----LFATVQANATDEDEEEELESVQRSVVGSIQASMEGSG 79
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                                                                                                                      10 KIISAGLVTASTATIVAGFSGVAMGAVMQYNRT
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                                      Indels 266;
                                                                                                                                                                                                                                                                                                                                                                                                               --GVKTGSTTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKD-
  DB 1; Length 1645;
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Rickettsiaceae; Rickettsieae; Rickettsia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---STDEG----EGLVTAKEVIDAVNKAGWRMKTTTANGQT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      543 AIGGGTYRGEAGYAIGYSSISDGGNWIIKGTASGNSRGHFGASASVG
                                        251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 -LNNRIDNVDGNAR-----AGIAQAIATAGLV----
; Score 186; DB
; Pred. No. 0.04
88; Mismatches
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                     21.1%;
                                            Conservative
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                         Similarity
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006653;
                                            Matches 162;
      Query Match
                           Best Local
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P38536;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                        999
                                                                                                                                                                                                                                                                                                                   APU_THETU
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                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                                                                                                                                409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     408 NVSPSK---GKMDETVN----IN---AGNN--IEISRNGKNIDIATSMAPQ----FSSV 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 VYTLKAGDNLKIKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410 TVPDTMTL-----TGNFTGDANNPGNTAGVITFAAN-GTLASASADANVAVTNNITA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 VESKDNG------KRTEVKIGAKTSVIKEKDGKLVTGK------GKGENGSSTDEGE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 IEASGVGVVQLSGTHTAELRLGNAGSVFKLADGTVINGKVNQTVLVGGVLAAGAITLDGS 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQ 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 GLVTAKEVIDAVNKAGWR--MKTTTANGQTGQADKFETVT-----SGTNVTFASGK 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 GTTATVSKDDQGNITVMYDV-----NVGDALNVNQLQNSGWNLDSKAVAGSSGKVISG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     571 GTIKLTS--TQNNIVVDCDLAIATDQTGVVDASSLT-----NAQTLTISGTIGIIGAN 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     622 NTTLGQFNIGSSKTTLNGGNVAINELVIGNNGSVQFAHNTYLITRTTNAAGQGKIIFNPV 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 TVQANATDEDEEEELES-----VQRSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYI 100
                                                                                                                                                                                                                                                                                          -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 GLNFAKETAGTNGDTTV-HLNGIGSTLTDTLAGSSASHVDAGNQSTHY-----TRAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     521 ATITG----DIGNGGGGAALQSITLAN-----DATKTLTLGGANIISANGGTINFQANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 -LIANAGPANAVIGTNNGAGRAAGFVVSVD--------NGKAATIDGQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           352 AKDMVIQSANANGQVNFRHIVDVG--IDGTTAFKTAASIVAITQNSNFGTTDFGNLAAQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 TINFNGTDGTGRLVLLSKNGAATDFNVTGSLGGNLKGIIELNTVAINGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 SIKDVLNAGWNIKGVKTGSTTGQSEN-----VDFVRTYDTVEFLSADTKTTTVN----
                                                                                                                        'Sequencing of the gene encoding the protein rOmp B of Rickettsia
                                                                                                                                        Japonica.";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 KDA SURFACE-EXPOSED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 KDA BETA PEPTIDE.
POLY-GLY.
W; 3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.2%; Score 185.5; DE 22.0%; Pred. No. 0.051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB003681; BAA20138.1; -.
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168097 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antigen; S-layer; Cell wall.
CHAIN 1339 1656
CHAIN 1339 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    528 53
1656 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                               SEQUENCE FROM N.A.
NCBI_TaxID=35790;
                                                                                                                                                                                                                                                                      SIMILARITY).
                                                                                                  Uchiyama T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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  NA RABA NA RAB
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                                                                                                                                                                   726 YATN-ITTTDAN----VGSFVFNAG------GKNIVS---GTVGGQQGNKFNIVALDNG 770
Clostridium thermosulfurogenes): molecular analysis of the gene, composite structure of the enzyme, and a common model for its attachment to the cell surface.";

J. Bacteriol. 176:3295-3302(1994)

CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides.

Linkages in oligosaccharides and polysaccharides.

Linkages in pullulan and in amylopectin and glycogen, and the alpha-and beta-limit dextrins of amylopectin and glycogen, and the slopa-and beta-limit dextrins of amylopectin and glycogen.

SLAYER ANCHOR.

PTW. GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-077-1994 (Rel. 30, Created)
01-070-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase type II) [Includes: Alpha-amylase (EC 3.2.1.1) (1.4-alpha-D-glucan glucanohydrolase); Pullulanase (EC 3.2.1.1) (1.4-alpha-D-glucan glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
                                                                                                                  NLNNRIDNVDGNARAGIAQAIATAGLVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matuschek M., Burchhardt G., Sahm K., Bahl H.; "Pullulanase of Thermoanaerobacterium thermosulfurigenes EM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoanaerobacter thermosulfurogenes (Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoanaerobacter group; Thermoanaerobacterium NCBI_TaxID=33950;
                                                                                                                                                                                                                                                                         -----GNWIIKGTA-----SGNSRGHFGASA 586
                                                                                                                                                                                                                                                                                                                                               771 TTVKFLGNATFNGNTTIAANSTLQISGNYTADFIASA 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed, entities requires a license agreement (See hor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1861 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004185; alpha-amylase_N.
InterPro; IPR004193; isoamylase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000461; Alpha_amylase.
InterPro; IPR003961; FN_III.
InterPro; IPR001119; SLH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-amylase_N; 1. fn3: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=DSM 3896 / EM1;
MEDLINE-94252998; PubMed-8195085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00128; alpha-amylase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF02806; alpha-amylase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             isoamylase_N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLH;
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Burland V.,

subdivision; Enterobacteriaceae;

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MEDLINE=97426617; PubMed=9278503; Batther F.R., Parna N.T., Burland V. Batther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical protein ydbA. TDBA OR B1401/R1405.
                                                      Bacteria; Proteobacteria; gamma
                                                                                                       SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                          Escherichia coli
                                                                               NCBI_TaxID=562;
                                                                 Escherichia
     29;
                                                                                                                                                                                                                                                                                                                                                                                                      1387 VTINGDSFVQDKNGV-FTKDVSLNYGVNKIKIHVEPNDGSVYGNDQGRITELTKDIEIDV 1445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGVITKNGNVITLTLDAGK-----AKDLIVNSKDKKVVFDITTIGEGQQ-----KV 1540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1604 VVDITISGISGNV------TLAKPVEVTLNISK--ANDPRKVAVYY 1641
                                                                                                                                                                                                                                                                                                             1208 NEVYNYIDTSVINGVTYNYKVVAVDLSFNRTESNVVTIKPDVVPIKVIFNVTVPDXTPDA 1267
                                                                                                                                                                                                                                                                                                                                                             1268 VNLAGTFPNATWDPSAQQMTKIDNNTY-SITLILDEGTQIEYKYARGSWDKVEKDEYGNE 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : : | : | : | : | : | : | : | IRQENNSGSGTGNINNTS-----TSGSNSSTGSGSTGSTSTTSNISNTSNT 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----IVIKSDNA 1565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1566 SIAL----TKDALNQNQIQN-GVNVSIK-------DNGKPNVTNYVSLSN 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LVTAKEVIDAVNKAGWRMKTTTANGQTGQADKFETVTSGTNVTFASGKGTTATVSKDDQG 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----TNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIAT 528
                                                                                                                                                                                                                                                                                                                                                                                       95 FVDPYIVVTLKAGDN-LKIKQNTNENTNASSFTYSLKKDLTGLINVETEKLSFGA-NGKK 152
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                      94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 AGLVQA----YLPGKS-----MMAIGGGTYRGEAGYAIGYSSISDGGNW 568
                                                                                                                                                                                                                                                                                                                                        -----NATDEDEEEELESVQRSVVGSIQASMEGSGELE-----TISLSMTNDSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSADTKTTTVNVESKDNGKRTEVKIGAKTSVIKEKDGKLV---TGKGKGENGSSTDEGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1642 YNPTINQWEYVGGKVDASSGIITFNATHFSQY - - AAFEYDKTFNDIKDNWAKDVIEVLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                          VNI-----ISDTKGLNFAKETA---GTN-----GDTTVHLNGIG--STLT-----DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 LAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNIKGVKTGSTTGQSENVDFVRTYDTVEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVISGNVSPSKGKMDETVNINAGN
              PROSITE; PSO1072; SLH_DOMAIN; 3.
Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;
Multifunctional enzyme; Glycoprotein.
                                                                                                                                                                                                                                                             Indels 205;
                                                                                                                                                                                                                                    Length 1861;
                                                                                                                                                                                                                                                                                      NKIYRIIWNSALNA-----WVAVSELTRNHTKRASATVKTAVLATLLFATVQA----
                                                                                                                                                                                    • E (IN REF. 1; AAB00841).
06C23070E453B574 CRC64;
                                                      POTENTIAL.
AMYLOPULLULANASE.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                   6.1%; Score 181.5; DB 1;
19.5%; Pred. No. 0.093;
tive 98; Mismatches 226;
                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
SLH 1.
SLH 2.
SLH 3.
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43;

YDBA\_ECOLI STANDARD; PRT; 2003 AA. P3366; P76087; P76088; P78859; 01-F8B-1994 (Rel. 28, Created) 16-OCT-2001 (Rel. 40, Last sequence update)

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Crocquet-Valdes P.A., Welss K., Walker D.H.;
Sequence analysis of the 190-kDa antigen-encoding gene of
conorii (Malish 7 strain).";
Gene 140:115-119(1994).
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Rickettsiaceae; Rickettsieae; Rickettsia
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D -> A (IN STRAINS INDIAN TICK TYPHUS, MI
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N -> H (IN STRAIN MOROCCAN).

M -> I (IN STRAIN INDIAN TICK TYPHUS).

Q -> K (IN REF. 1).

I -> V (IN REF. 1).

V -> I (IN REF. 1).

G -> D (IN REF. 1).
                                                                                                                     STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan; MEDLIFE-97015921; PubMed-886258; Roux V., Fournier P.E., Raoult D.; "Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rompA."; Clin. Microbiol. 34:2058-2065(1996).
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KATLGGAIIKATTTK -> LLQVQGGVVKANTIN (IN
"Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
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STRAIN-Indian tick typhus, MI, Malish 7, and Moroccan;

STRAIN-Indian tick typhus, MI, Malish 7, and Moroccan;

Staoult D., Fournier P.E., Roux V.;

"Phylogenetic analysis of spotted fever group rickettsiae by st

of the outer surface protein rompA.";

Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).

-! SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED

S-LAYER WITH HEXAGONAL SYMMERRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -! - SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY
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Pfan; PF02708; rOmpA_rOmpB; 1.
Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein; Complete proteome.
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U43794; AAB49549.1; -.
U43798; AAB49550.1; -.
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                                                                                             SEQUENCE OF 8-204 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 IQASMEGSGELETISLSMTNDSK---EFVDPYIVVTLKAG-----DNLKIKQNTNENT- 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 TFASGKGTTATVSK--DDQGNITVMYDVNVGDALNVNQLQNSGWNLDSKAVAGSSGKVIS 406
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   LLRVQGGVVKSNTIN -> KATLGGAIIKATTTK (IN
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